

SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
Date: _____ Phone: _____ Art Unit: _____

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 07-07-04
Searcher: Beverly E 2528
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

_____ STIC
_____ CM-1
_____ Pre-S

Type of Search

_____ N.A. Sequence
_____ A.A. Sequence
_____ Structure
_____ Bibliographic

Vendors

_____ IG
_____ STN
_____ Dialog
_____ APS
_____ Geninfo
_____ SDC
_____ DARC/Questel
☒ Other CGN

STIC-Biotech/ChemLib

126063

From: Ramirez, Delia
Sent: Wednesday, June 30, 2004 11:45 AM
To: STIC-Biotech/ChemLib
Subject: case 09/762,258

Hi,

I would like to request the following interference search:

1. seq id 1 and 2 in the nucleic acid databases
2. seq id 2 in the protein databases

Thank you,

Delia M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
400 Dulany Street, Remsen Bldg., 3A74, Mail room 3C70
Alexandria, VA 22314
(571) 272-0938
delia.ramirez@uspto.gov

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Searcher: _____
Phone: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

QY 361 CLOSEBVSQDPTFTQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSQPK 420
 DB 361 CLOSEBVSQDPTFTQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSQPK 420
 QY 421 LRSRRRLNSSRRVSVSLKSPFGRFSPSLPPTLPLPPLPPPPSTTAPLTPRP 480
 DB 421 LRSRRRLNSSRRVSVSLKSPFGRFSPSLPPTLPLPPLPPPPSTTAPLTPRP 480
 QY 481 SGTCKSKRGGRGPR 495
 DB 481 SGTCKSKRGGRGPR 495

RESULT 2
 US-09-430-564-2
 ; Sequence 2, Application US/09430564
 ; Patent No. 6372467
 ; GENERAL INFORMATION:
 ; APPLICANT: John Blenis
 ; APPLICANT: Kay K. Lee-Fruman
 ; APPLICANT: Calvin J. Kuo
 ; TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
 ; FILE REFERENCE: 00246/506002
 ; CURRENT APPLICATION NUMBER: US/09/430,564
 ; PRIOR FILING DATE: 1999-10-29
 ; PRIOR APPLICATION NUMBER: 60/106,141
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 482
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-430-564-2

Query Match 97.6%; Score 2551; DB 4; Length 482;
 Best Local Similarity 100.0%; Pred. No. 7,2e-204;
 Matches 482; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MAAYFDLDLTERGSGEGEPBESPADACPLAELRAAGLPRVGHVEBELTETSVNGPE 73
 DB 1 MAAYFDLDLTERGSGEGEPBESPADACPLAELRAAGLPRVGHVEBELTETSVNGPE 60
 QY 74 RIGPHCELLRYLKGKGYGVFQVRKVOGNTLGIYAMKYLRAKIVANAKDTAHTRAR 133
 DB 61 RIGPHCELLRYLKGKGYGVFQVRKVOGNTLGIYAMKYLRAKIVANAKDTAHTRAR 120
 QY 134 NILESVAHPPIVELAAYAFOTGKLYILBCLSGGELFTLBRGIFLEDTACFYLAETL 193
 DB 121 NILESVAHPPIVELAAYAFOTGKLYILBCLSGGELFTLBRGIFLEDTACFYLAETL 180
 QY 194 ALGHLSOGITVDLPEENIMSSOGHITLDTGCLCKESIHGAVHTTCGITEVAPPI 253
 DB 181 ALGHLSOGITVDLPEENIMSSOGHITLDTGCLCKESIHGAVHTTCGITEVAPPI 240
 QY 254 LVASGNRAVDWMSLALMYDMLTGSPPFAENRKKTXMDXIRGKALAPPIYLPDARDLV 313
 DB 241 LVASGNRAVDWMSLALMYDMLTGSPPFAENRKKTXMDXIRGKALAPPIYLPDARDLV 300
 QY 314 KXFLKNPQORIGGGGADADVORHPPFTAMMDLLARVDPFPFPCLOSEEDVSQFDT 373
 DB 301 KXFLKNPQORIGGGGADADVORHPPFTAMMDLLARVDPFPFPCLOSEEDVSQFDT 360
 QY 374 RFRQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSQPKLSPRLNSSPRV 433
 DB 361 RFRQTPVDSDDTALSESANQALGFTYVAPSLDSIKGFSQPKLSPRLNSSPRV 420
 QY 434 PVSPLKSPFGRFSPSLPPTLPLPPLPPPPSTTAPLPIRPSGTTKSKRGGRP 493
 DB 421 PVSPLKSPFGRFSPSLPPTLPLPPLPPPPSTTAPLPIRPSGTTKSKRGGRP 480

QY 494 GR 495
 DB 481 GR 482

RESULT 3
 US-08-749-902-8
 ; Sequence 8, Application US/08749902
 ; Patent No. 5985635
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/749,902
 ; FILING DATE: Filed Herewith
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0150 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 525 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: 1562
 ; US-08-749-902-8

Query Match 66.9%; Score 1749; DB 2; Length 525;
 Best Local Similarity 68.2%; Pred. No. 3.6e-137;
 Matches 350; Conservative 51; Mismatches 82; Indels 30; Gaps 8;

QY 1 MARGRRAGAGAA-----MAAYFDLDLTERGSGEGEPBESPADACPLAE-LRA 49
 DB 1 MARRRRBQFPAPDPFRBAEDMAGVFDLDQPEDAGSDELE---EGQLNBSMDH 56
 QY 50 AGLEB---VGHVEBELTETSVNGPERIGPHCELLRYLKGKGYGVFQVRKVOGNTL 105
 DB 57 GGVGPEYELGMEHCEPEISFETSVNGPKIRPECELLRYLKGKGYGVFQVRKVOGNTL 116
 QY 106 GKIYAMKYLRAKIVANAKDTAHTRAENILSVHPPIVELAAYAFOTGKLYILBCL 165
 DB 117 GKIYAMKYLRAKIVANAKDTAHTRAENILSVHPPIVELAAYAFOTGKLYILBCL 176
 QY 166 GGEFLTHLRGCIPLIEDTACCTAATLALGHLHSGITVDLPEENIMSSOGHITL 225
 DB 177 GGEFLTHLRGCIPLIEDTACCTAATLALGHLHSGITVDLPEENIMHGHVKTLD 236
 QY 226 FGLCKESIHGAVHTTCGITEVAPPIYLVASGNRAVDWMSLALMYDMLTGSPPFAE 285


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Db 237 FGLCKESIHGDTVHTTCGILTYMAPEILKSGNRAVDWMSLGALMTDLTGAPEPTGE 236
Qy 286 NRKKTMDKIRGKIALPPYLTPDARDLVKFKLRNPSQRIQGGPGDAADVQRRPFRHNN 345
Db 297 NRKKTIDKIKCKMLPPYLTOEARDLKLLKNNASRLGAGPGDAGVQAHPPFRHIN 356
Qy 346 MDLLAMRVDPFPPRCLQSEEDVSGQPTFRTPROTVPVSPDDTALSANQAFLGFTYVAP 405
Db 357 WEELAKRVBPFRKPLQSEEDVSGQSKFTROTVPVSPDDSTLSANQVFLGFTYVAP 416
Qy 406 SVLDSIKEGSFQPKLRSPRLNNSPRVVSPLKFSPE---GFRPSPLPR-PTLPL 460
Db 417 SVLESVKEKFSFPRKIRSPRRFGSPRTVPVSPVKFSFGDFMGASASTANPQTPVEYPM 476
Qy 461 PLPPPPSPST-----APLPIRP-SGTKSK 487
Db 477 ETSGIEQMDVTTSGEASAPLPIRQPNSSPYKKQ 509

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RESULT 4

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US-08-749-902-7
Sequence 7, Application US/08749902
Patent No. 5985635
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Goll, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: US
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/749,902
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0150 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 525 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONING: 189508
US-08-749-902-7

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Query Match 66.8%; Score 1747; DB 2; Length 525;
Best Local Similarity 67.9%; Pred. No. 5.2e-137;
Matches 351; Conservative 49; Mismatches 79; Indels 38; Gaps 8;

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Qy 1 MARGRRARAGAA-----MAAVFDLLETBEGSGEGPPLSPADACPLAE-LRA 49

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Db 1 MRRRRRDGFYAPDRDRAEMAGVFDIDDQPEPDASSEDELE-----EGGQLNESKDH 56
Qy 50 AGLRP-----VGHYEVELTETSVNNGPERIGPHCFELLVLAGKGYGVKVPVRKVGQTNL 105
Db 57 GGVGPEYELQMEHCHEKEKEISSETSVNRGPEKIRPECFELILVLGKGYGVKVPVRKVGANT 116
Qy 106 GKIYAKVLRKAKIVANAQDTHATRAERNILSVKRPFLVEILAYAFQTGKLYLILEGSL 165
Db 117 GKIFANKVLRKAKIVANAQDTHATRAERNILSVKRPFLVEILAYAFQTGKLYLILEGLS 176
Qy 166 GSELFTHLRREGIFLEDACFYLAITLALGHLSGIIYRDKPENIMLSGGHILKLD 225
Db 177 GSELFTHLRREGIFLEDACFYLAITLALGHLSGIIYRDKPENIMLSGGHILKLD 236
Qy 226 FGLCKESIHGAVTHTFCCTIETMAPEILYRSGHRAVQWMSLGALMYKLTGAPPTFA 285
Db 237 FGLCKESIHGDTVHTTCGILTYMAPEILYRSGHRAVQWMSLGALMYKLTGAPPTFA 296
Qy 286 NRKKTMDKIRGKIALPPYLTPDARDLVKFKLRNPSQRIQGGPGDAADVQRRPFRHNN 345
Db 297 NRKKTIDKIKCKMLPPYLTOEARDLKLLKNNASRLGAGPGDAGVQAHPPFRHIN 356
Qy 346 MDLLAMRVDPFPPRCLQSEEDVSGQPTFRTPROTVPVSPDDTALSANQAFLGFTYVAP 405
Db 357 WEELAKRVBPFRKPLQSEEDVSGQSKFTROTVPVSPDDSTLSANQVFLGFTYVAP 416
Qy 406 SVLDSIKEGSFQPKLRSPRLNNSPRVVSPLKFSPE---FEGFRPSPLPPTLPLPL 463
Db 417 SVLESVKEKFSFPRKIRSPRRFGSPRTVPVSPVKFSFGDFMGASAS-----TANPQTPV 472
Qy 464 LPPPPS-----TAPLPIRP-SGTKSK 487
Db 473 EYFMETSGIEQMDVTTSGEASAPLPIRQPNSSPYKKQ 509

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RESULT 5

```

US-09-430-564-16
Sequence 16, Application US/09430564
Patent No. 6372467
GENERAL INFORMATION:
APPLICANT: John Blenis
APPLICANT: Kay K. Lee-Fruman
APPLICANT: Calvin J. Kuo
TITLE OF INVENTION: P54S6K AND P8S6K GENES, PROTEINS,
FILE REFERENCE: 00246/506002
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,564
FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,141
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 16
LENGTH: 525
TYPE: PRT
ORGANISM: Homo sapiens
US-09-430-564-16

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Query Match 66.8%; Score 1747; DB 4; Length 525;
Best Local Similarity 67.9%; Pred. No. 5.2e-137;
Matches 351; Conservative 49; Mismatches 79; Indels 38; Gaps 8;

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Qy 1 MARGRRARAGAA-----MAAVFDLLETBEGSGEGPPLSPADACPLAE-LRA 49
Db 1 MRRRRRDGFYAPDRDRAEMAGVFDIDDQPEPDASSEDELE-----EGGQLNESKDH 56
Qy 50 AGLRP-----VGHYEVELTETSVNNGPERIGPHCFELLVLAGKGYGVKVPVRKVGQTNL 105
Db 57 GGVGPEYELQMEHCHEKEKEISSETSVNRGPEKIRPECFELILVLGKGYGVKVPVRKVGANT 116
Qy 106 GKIYAKVLRKAKIVANAQDTHATRAERNILSVKRPFLVEILAYAFQTGKLYLILEGSL 165
Db 117 GKIFANKVLRKAKIVANAQDTHATRAERNILSVKRPFLVEILAYAFQTGKLYLILEGLS 176

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QY 166 GGEFTHERBEGFLBETACPYLAITLALGHASGGIITRDLPENIMLSSGGHITLND 225
 DB 177 GGEFTHERBEGFLBETACPYLAITLALGHASGGIITRDLPENIMLSSGGHITLND 236
 QY 226 FGLCKESIHEGAVTHTCGTEIYVAPFELVRSGNRAVDMWSLALYDMLTJGSPPTAE 285
 DB 237 FGLCKESIHEGAVTHTCGTEIYVAPFELVRSGNRAVDMWSLALYDMLTJGSPPTAE 296
 QY 286 NRKXTMDKIRKXALPPLYLPDARDLVKKFLKRNPSQRIQGGPGDAADVQRHFFRHMN 345
 DB 297 NRKXTMDKIRKXALPPLYLPDARDLVKKFLKRNPSQRIQGGPGDAADVQRHFFRHMN 356
 QY 346 WDLIARVDPPEPFCLOSEEDVSQFDRFTRCPVNSPDITLSBANAFLGFTYVAP 405
 DB 357 WDLIARVDPPEPFCLOSEEDVSQFDRFTRCPVNSPDITLSBANAFLGFTYVAP 416
 QY 406 SVLDSINEGFSFOKXSPRRLNSSPRVPSPLKFSF--FEGFRPSPLPEPTELPPL 463
 DB 417 SVLDSINEGFSFOKXSPRRLNSSPRVPSPLKFSF--FEGFRPSPLPEPTELPPL 472
 QY 464 LPPPPS-----TTAPPIPP--SGTKSK 487
 DB 473 EYMETSGIEQMDVTWSGASAPLPIRQNSGPKXQ 509

RESULT 6

US-09-817-310-2
 ; Sequence 2, Application US/09817310
 ; Patent No. 6534311
 ; GENERAL INFORMATION:
 ; APPLICANT: Stewart, Mary
 ; APPLICANT: Kozma, Sarah
 ; APPLICANT: Thomas, George
 ; TITLE OF INVENTION: Drosophila melanogaster P70 S6 Kinase
 ; FILE REFERENCE: 4-20371/A
 ; CURRENT APPLICATION NUMBER: US/09/817,310
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 09/230,247
 ; PRIOR FILING DATE: 1999-04-16
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 637
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-817-310-2

Query Match 54.6%; Score 1428; DB 4; Length 637;
 Best Local Similarity 67.2%; Pred. No. 2.2e-110;
 Matches 279; Conservative 47; Mismatches 81; Indels 8; Gaps 4;

QY 19 DLDLETEGSEGESE-ELSPADACPLAEPLRAAGLEPVGHYEVELETETSVNVPRIOP 77
 DB 17 DLDLETEGSEGESE-ELSPADACPLAEPLRAAGLEPVGHYEVELETETSVNVPRIOP 74
 QY 78 HCEFLRLVTLGKGYGVQVRKVGQTNLGIYAMKYLKAKIYRNADOTATRAERNILIE 137
 DB 75 KDBELKVLGKGYGVQVRKVGQTNLGIYAMKYLKAKIYRNADOTATRAERNILIE 134
 QY 138 SVHGFPIVELAVAFOTGKLYLLECLSGGELFTHERBEGFLBETACPYLAITLALGH 197
 DB 135 AVHGFPIVELAVAFOTGKLYLLECLSGGELFTHERBEGFLBETACPYLAITLALGH 194
 QY 198 LHSOGIITRDLPENIMLSSGGHITLDPGLCKESIHEGAVTHTCGTEIYVAPFELVRS 257
 DB 195 LHSOGIITRDLPENIMLSSGGHITLDPGLCKESIHEGAVTHTCGTEIYVAPFELVRS 254
 QY 258 GHNRAVDWMSLALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYLPDARDLVKKFL 317
 DB 255 GHNRAVDWMSLALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYLPDARDLVKKFL 314
 QY 318 KRNPSQRIQGGPGDAADVQRHFFRHMNDLILAMRVDPPEPFCLOSEEDVSQFDRFTR 377

DB 315 KQEPFRLSGGPDAAVQIHPPFKHVNMDVLARLEPPIKPLKSEEDVSQFDRFTR 374
 QY 378 QTPVSPDDTALSANQAFGLFTYVAPSVLDSIKGFSFOKXSPRRLNSSPR 432
 DB 375 QTPVSPDDTALSANQAFGLFTYVAPSVLDSIKGFSFOKXSPRRLNSSPR 424

RESULT 7

US-09-430-564-12
 ; Sequence 12, Application US/09430564
 ; Patent No. 6372467
 ; GENERAL INFORMATION:
 ; APPLICANT: John Blenis
 ; APPLICANT: Kay K. Lee-Fruman
 ; APPLICANT: Calvin J. Kuo
 ; TITLE OF INVENTION: P54SK AND P85SK GENES, PROTEINS,
 ; FILE REFERENCE: 00246/506002
 ; CURRENT APPLICATION NUMBER: US/09/430,564
 ; CURRENT FILING DATE: 1998-10-29
 ; PRIOR APPLICATION NUMBER: 60/106,141
 ; PRIOR FILING DATE: 1998-10-29
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 268
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-430-564-12

Query Match 54.1%; Score 1415; DB 4; Length 268;
 Best Local Similarity 100.0%; Pred. No. 8.3e-110;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 HCEFLRLVTLGKGYGVQVRKVGQTNLGIYAMKYLKAKIYRNADOTATRAERNILIE 137
 DB 1 HCEFLRLVTLGKGYGVQVRKVGQTNLGIYAMKYLKAKIYRNADOTATRAERNILIE 60
 QY 138 SVHGFPIVELAVAFOTGKLYLLECLSGGELFTHERBEGFLBETACPYLAITLALGH 197
 DB 61 SVHGFPIVELAVAFOTGKLYLLECLSGGELFTHERBEGFLBETACPYLAITLALGH 120
 QY 198 LHSOGIITRDLPENIMLSSGGHITLDPGLCKESIHEGAVTHTCGTEIYVAPFELVRS 257
 DB 121 LHSOGIITRDLPENIMLSSGGHITLDPGLCKESIHEGAVTHTCGTEIYVAPFELVRS 180
 QY 258 GHNRAVDWMSLALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYLPDARDLVKKFL 317
 DB 181 GHNRAVDWMSLALYDMLTJGSPPTAENRKKTMKXIRGKALPPLYLPDARDLVKKFL 240
 QY 318 KRNPSQRIQGGPGDAADVQRHFFRHMN 345
 DB 241 KRNPSQRIQGGPGDAADVQRHFFRHMN 268

RESULT 8

US-08-749-902-3
 ; Sequence 3, Application US/08749902
 ; Patent No. 5985635
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Goli, Surya K.
 ; APPLICANT: Hillman, Jennifer L.
 ; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: INCYTE PHARMACEUTICALS, INC.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: US

ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION NUMBER: US/08/749, 902
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0150 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 495 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: Consensus
US-08-749-902-3

Query Match 53.0%; Score 1385.5; DB 2; Length 495;
Best Local Similarity 61.7%; Pred. No. 5.3e-107;
Matches 282; Conservative 39; Mismatches 75; Indels 61; Gaps 9;

86 LGKGGVGVQVRKQGTNL--GKIVAMKYL-----KAKIVNAKDTAHTAERNILE 137
43 LGSAHARVQRC-----INLITSOEYXVXIIIFPKGHIRSVREVEMLYQCGGHRVLE 97
138 SVKHPFIVELAYAFQTGKLYLILECLSGGELFTHLERBGIFLEDTACFYLAETITLALGH 197
98 LIEF-----FEEDRFYLVFEKVRGGSILSHIKRRHFELASVVVQVVASALDF 148

198 LHSQGIYRDLPKRNIMLSSQGH---IKLDFGLCKESIHEGAVTH-----TFGGTIR 247
149 LHNKGIAHRLDKPENILCGRPNQVSPVKIDFDLGGSGIKLNGCSPISTRELLTFCGSAR 208
248 YMAPEI-----LVSSGHRVAD--WMS---LGALMYDMLTG 278
209 YMAPVEVEAFSEASITDKKCDLMSGLVILIISGIPPPVGRMQRRLRGLPTMYMLTG 268
279 SPPTAENRKTMDKIIIRGKLALPPYITPDARDLVKKFLKRNPSQRIIGGPGDADVQGRH 338
269 SPPTAENRKTMDKIIIRGKLALPPYITPDARDLVKKFLKRNPSQRIIGGPGDADVQGRH 328
339 PFRHNMMDLLMARVDPFRPCLOSEEDVSQFTPTROTVPDSDDDTLASNAQAF 398
329 PFRHNMMDLLMARVDPFRPCLOSEEDVSQFTPTROTVPDSDDDTLASNAQAF 388
399 GFTYVAPSVLDSIKEGFSFQPKLRSRRRLNSSPRVPSPLKFSFGFRSPSPSPETEL 458
389 GFTYVAPSVLDSIKEGFSFQPKLRSRRRLNSSPRVPSPLKFSFGFRSPSPSPETEL 448
459 PLPPLLPPTPTTAPLPFRPSTGKSKRGGRGRGR 495
449 PLPPLLPPTPTTAPLPFRPSTGKSKRGGRGRGR 485

RESULT 9
US-09-430-564-6
Sequence 6, Application US/09430564
Patent No. 6372467
GENERAL INFORMATION:
APPLICANT: John Blenis
APPLICANT: Kay K. Lee-Fruman

APPLICANT: Calvin J. Kuo
TITLE OF INVENTION: P54S6K AND P85S6K GENES, PROTEINS,
FILE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
FILE REFERENCE: 00246/506002
CURRENT APPLICATION NUMBER: US/09/430, 564
CURRENT FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/106,141
PRIOR FILING DATE: 1998-10-29
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 258
TYPE: PRP
ORGANISM: Homo sapiens
US-09-430-564-6

Query Match 51.8%; Score 1354; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 9.2e-105;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

78 HCEELRLVLAGGGYGVQVRKQGTNLGKIVAMKYLRAKIVNAKDTAHTAERNILE 137
1 HCEELRLVLAGGGYGVQVRKQGTNLGKIVAMKYLRAKIVNAKDTAHTAERNILE 60
138 SVKHPFIVELAYAFQTGKLYLILECLSGGELFTHLERBGIFLEDTACFYLAETITLALGH 197
61 SVKHPFIVELAYAFQTGKLYLILECLSGGELFTHLERBGIFLEDTACFYLAETITLALGH 120

198 LHSQGIYRDLPKRNIMLSSQGHIIKLTDFGLCKESIHEGAVTHTFGGTIRYMAPEILVRS 257
121 LHSQGIYRDLPKRNIMLSSQGHIIKLTDFGLCKESIHEGAVTHTFGGTIRYMAPEILVRS 180
258 GHRNAVDMWSLALAMVDMLTGSPPTAENRKTMDKIIIRGKLALPPYITPDARDLVKKFL 317
181 GHRNAVDMWSLALAMVDMLTGSPPTAENRKTMDKIIIRGKLALPPYITPDARDLVKKFL 240

318 KNPSSQRIIGGPGDADV 335
241 KNPSSQRIIGGPGDADV 258

RESULT 10
US-09-031-295-2
Sequence 2, Application US/09031295
Patent No. 6326181
GENERAL INFORMATION:
APPLICANT: LANG, Florian
TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031, 295
FILING DATE: 26-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 197-08-173, 8
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 058315/0123

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-031-295-2

Query Match 30.9%; Score 806.5; DB 4; Length 431;
Best Local Similarity 44.3%; Pred. No. 5,7e-59;
Matches 172; Conservative 66; Mismatches 111; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEIRAAGLPEVGHVEVELTETSVNNGPERIGPHC---PELLRVLCX 88
DB 65 EPELNNANPSP-----PPSPSQ-----INIGPSS-NPHAKPSDFHFLKVIQK 106
QY 89 GGKGVKPVQR-KVQGTNLGKIYAMKYLAKKIVRAKDTAFTAAERNI-LESVKHPIYE 146
DB 107 GSGKVLARHKAEEV---FYAVKVLQKALIKK-KBKHMSEKRVNLKVKHPIFLVG 161
QY 147 IAAVAFQSGKLYLIECLSGSELTFLHREGIFLEDYACFYLAETTLALGHLHSGGIYR 206
DB 162 LHSFQPADKLYFLVDYINGELFYHLQRECFLEPRARVAAEIASALGYLHSLNIYR 221
QY 207 DKPENIMLSQGHKLTDFGCKESIHGAVTHTFCGTEVMAPEILVRSGHNRADVW 266
DB 222 DLKPEHILDSQGHVLTDFGCKENIENHSTSTFCGTEVMAPEILVRSKHQPDYDWM 281
QY 267 SIGALMYDMLTGSPPFTAEKRRKTKMDKIRGKLLPPLYLPDARDLVKPELRNPDSQIG 326
DB 282 CLGAVLYEMLYGPPFYSRNTAEMTDNINKPLQKPNITNSARHLBGLQKDKTKRL- 340
QY 327 GGGGDAADVQRPPFRHNMMDLLAMRVDPFRPCLQSEEDVSQPTRETRQTPV----- 381
DB 341 GAQDPMETKSHVFFSLINMDDLINKKLTPEPNVSGPMDLRHPDPETEE-PVPNSIG 399
QY 382 DSPDD---TALSESANOAFLETTYAPS 406
DB 400 KSPDSVLTASVKEAAEAFLEGSYAPPT 427

RESULT 11

US-08-712-709-5
Sequence 5, Application US/08712709
Patent No. 5663780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herein
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy U
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-08-712-709-5

Query Match 30.7%; Score 802.5; DB 2; Length 431;
Best Local Similarity 44.3%; Pred. No. 1.2e-58;
Matches 172; Conservative 65; Mismatches 112; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEIRAAGLPEVGHVEVELTETSVNNGPERIGPHC---PELLRVLCX 88
DB 65 EPELNNANPSP-----PPSPSQ-----INIGPSS-NPHAKPSDFHFLKVIQK 106
QY 89 GGKGVKPVQR-KVQGTNLGKIYAMKYLAKKIVRAKDTAFTAAERNI-LESVKHPIYE 146
DB 107 GSGKVLARHKAEEV---FYAVKVLQKALIKK-KBKHMSEKRVNLKVKHPIFLVG 161
QY 147 IAAVAFQSGKLYLIECLSGSELTFLHREGIFLEDYACFYLAETTLALGHLHSGGIYR 206
DB 162 LHSFQPADKLYFLVDYINGELFYHLQRECFLEPRARVAAEIASALGYLHSLNIYR 221
QY 207 DKPENIMLSQGHKLTDFGCKESIHGAVTHTFCGTEVMAPEILVRSGHNRADVW 266
DB 222 DLKPEHILDSQGHVLTDFGCKENIENHSTSTFCGTEVMAPEILVRSKHQPDYDWM 281
QY 267 SIGALMYDMLTGSPPFTAEKRRKTKMDKIRGKLLPPLYLPDARDLVKPELRNPDSQIG 326
DB 282 CLGAVLYEMLYGPPFYSRNTAEMTDNINKPLQKPNITNSARHLBGLQKDKTKRL- 340
QY 327 GGGGDAADVQRPPFRHNMMDLLAMRVDPFRPCLQSEEDVSQPTRETRQTPV----- 381
DB 341 GAQDPMETKSHVFFSLINMDDLINKKLTPEPNVSGPMDLRHPDPETEE-PVPNSIG 399
QY 382 DSPDD---TALSESANOAFLETTYAPS 406
DB 400 KSPDSVLTASVKEAAEAFLEGSYAPPT 427

RESULT 12

US-09-111-444-5
Sequence 5, Application US/09111444
Patent No. 6045792
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-111-444-5

Query Match 30.7%; Score 802.5; DB 3; Length 431;
Best Local Similarity 44.3%; Pred. No. 1.2e-58;
Matches 172; Conservative 65; Mismatches 112; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEALRAAGLEPVGHVEVELTETSVMVGPERRIGPHC---FELLRYLQK 88
DB 65 EPELMMANPSP-----PPSPSQ-----INLGPS-NPNAKPSDFHFLKVTGK 106
QY 89 GGYKVFQVR-KVQGTNLGKIYAMKVLRAKIVNAKDTAHTRAERNI-LESYKEPPIVE 146
DB 107 GSFQKYLARHKAERV---FYAVKVLQKAILKK-KEEKHIMSERVNLKVMHPELVG 161
QY 147 LAAVFOGSKYLIIECLSGSELFTHLEREGIFLEDTACFYLAETTLAIGHLSQCIYR 206
DB 162 LHPSFOADKLYFVLDYINGSELFTHLQRECEFLPRASVAAEIASALGYHSLNIVYR 221
QY 207 DLKPEINIMSSQGHILKLDGFCCKESIHEGAVTHFCGTEYMAPEILVRSCHNRADVW 266
DB 222 DLKPEINILDSQGHIVLIDFGLCENIENHSTSTFCGTEYLAPEVLHKOYDRIVDW 281
QY 267 SLGALMYDNLGSPPTAEMRKKTMDKIIRGKLALPYLTPDARDLVKKFLKRNPSQRIQ 326
DB 282 CLGAVLYEMLYGLPPFYSRNTAEMTDNINLKLPLQKENTINSARHLIEGLIQDRTKRL- 340
QY 327 GCGPDADVQRRHPPFRHNMWDLLAMRVDPFRPCLQSEEDVSGQDTRFTROTQPV----- 381
DB 341 GAKDDFMEIKSHVFPFLINWDLLINKKITPPNPVNSGENDLHAFDEFTER-PVPNSIG 399
QY 382 DSPDD---TALSASANQAFIGFTYVAPS 406
DB 400 KSPDSVLTASVKEAABAFIGFSVAPPT 427

RESULT 13
US-09-541-228-5
Sequence 5, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541,228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 431 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-541-228-5

Query Match 30.7%; Score 802.5; DB 3; Length 431;
Best Local Similarity 44.3%; Pred. No. 1.2e-58;
Matches 172; Conservative 65; Mismatches 112; Indels 39; Gaps 12;

QY 33 EPELSPADACPLAEALRAAGLEPVGHVEVELTETSVMVGPERRIGPHC---FELLRYLQK 88
DB 65 EPELMMANPSP-----PPSPSQ-----INLGPS-NPNAKPSDFHFLKVTGK 106
QY 89 GGYKVFQVR-KVQGTNLGKIYAMKVLRAKIVNAKDTAHTRAERNI-LESYKEPPIVE 146
DB 107 GSFQKYLARHKAERV---FYAVKVLQKAILKK-KEEKHIMSERVNLKVMHPELVG 161
QY 147 LAAVFOGSKYLIIECLSGSELFTHLEREGIFLEDTACFYLAETTLAIGHLSQCIYR 206
DB 162 LHPSFOADKLYFVLDYINGSELFTHLQRECEFLPRASVAAEIASALGYHSLNIVYR 221
QY 207 DLKPEINIMSSQGHILKLDGFCCKESIHEGAVTHFCGTEYMAPEILVRSCHNRADVW 266
DB 222 DLKPEINILDSQGHIVLIDFGLCENIENHSTSTFCGTEYLAPEVLHKOYDRIVDW 281
QY 267 SLGALMYDNLGSPPTAEMRKKTMDKIIRGKLALPYLTPDARDLVKKFLKRNPSQRIQ 326
DB 282 CLGAVLYEMLYGLPPFYSRNTAEMTDNINLKLPLQKENTINSARHLIEGLIQDRTKRL- 340
QY 327 GCGPDADVQRRHPPFRHNMWDLLAMRVDPFRPCLQSEEDVSGQDTRFTROTQPV----- 381
DB 341 GAKDDFMEIKSHVFPFLINWDLLINKKITPPNPVNSGENDLHAFDEFTER-PVPNSIG 399
QY 382 DSPDD---TALSASANQAFIGFTYVAPS 406
DB 400 KSPDSVLTASVKEAABAFIGFSVAPPT 427

RESULT 14
US-08-712-709-9
Sequence 9, Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

```

ADDRESSES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/712,709
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 294637
US-08-712-709-9

Query Match      30.3%; Score 791; DB 2; Length 430;
Best Local Similarity 44.4%; Pred. No. 1,1e-57;
Matches 174; Conservative 64; Mismatches 112; Indels 42; Gaps 14;

QY 33 EPEISPADACPLAELEAAGLEPVGHYEVEVLTETSVNGPERIGPHC---FELLRLVIGK 88
DB 65 EPELMANPSP-----PPSPSQ-----INLGPS--NPHAKSDHFLKLVIGK 106
QY 89 GGYGVKFOVR-KVQGTNLGKIYAMKVIKAKIVRNKDTAHTRAERNI-LESYKHPFIYE 146
DB 107 GSGFGVLLARHKAEEA---FYAVVYLOKKAILEK-KEEKIMSERNVLLKNVKAHPFLVG 161
QY 147 LAFAFOTGKLYLILECISGSELEFTHREGEIPLBPTACPYLAETITLALGHLHSGGIYR 206
DB 162 LHRSPQTADKLYFLVDYINGBELPYHLQRRRCFLERARFYAAELIASLGYHLSNIYTR 221
QY 207 DLKPEINMLSSQGHILKLDPLGCKESIHGCAVHTTFCGTIYMAPEIIVRSGENRAVDW 266
DB 222 DLKPEINMLSSQGHILKLDPLGCKENIENHGTSTFCGTPEYLAPEVILKQPYRTVDW 281
QY 267 SLGALMYDMLTSSPPFTAEKRTKMDKTIIRGKLLPVLTPDARDLVKPPFKBNPSQRI 326
DB 282 CLGAVLYEMLYGLPPFYSRNTAEMYNILAKPLQI-KNITNSAKHLBGLQOKRTKRL- 339
QY 327 GSGFGADAVQRRHPPFRHNMWDLAMRVDPFRPCLOSSEDDVSQDTRFTROTVD--- 382
DB 340 GAKDDEWEIKSHIFFSLINWDDLINKKITPPFPNPNVSGPSDLRHFDPFEETEE-PVPSISIG 398
QY 383 -SPDD---TALSASNAQFLGFTYVAPSVYDS 410
DB 399 RSPDSILVTASVKAEAELFGFSYAPP--WDS 428

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RESULT 15
 US-09-111-444-9
 Sequence 9, Application US/09111444
 Patent No. 6045792
 GENERAL INFORMATION:
 APPLICANT: Au-Young, Janice
 APPLICANT: Guegler, Karl J.

```

APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 294637
US-09-111-444-9

Query Match      30.3%; Score 791; DB 3; Length 430;
Best Local Similarity 44.4%; Pred. No. 1,1e-57;
Matches 174; Conservative 64; Mismatches 112; Indels 42; Gaps 14;

QY 33 EPEISPADACPLAELEAAGLEPVGHYEVEVLTETSVNGPERIGPHC---FELLRLVIGK 88
DB 65 EPELMANPSP-----PPSPSQ-----INLGPS--NPHAKSDHFLKLVIGK 106
QY 89 GGYGVKFOVR-KVQGTNLGKIYAMKVIKAKIVRNKDTAHTRAERNI-LESYKHPFIYE 146
DB 107 GSGFGVLLARHKAEEA---FYAVVYLOKKAILEK-KEEKIMSERNVLLKNVKAHPFLVG 161
QY 147 LAFAFOTGKLYLILECISGSELEFTHREGEIPLBPTACPYLAETITLALGHLHSGGIYR 206
DB 162 LHRSPQTADKLYFLVDYINGBELPYHLQRRRCFLERARFYAAELIASLGYHLSNIYTR 221
QY 207 DLKPEINMLSSQGHILKLDPLGCKESIHGCAVHTTFCGTIYMAPEIIVRSGENRAVDW 266
DB 222 DLKPEINMLSSQGHILKLDPLGCKENIENHGTSTFCGTPEYLAPEVILKQPYRTVDW 281
QY 267 SLGALMYDMLTSSPPFTAEKRTKMDKTIIRGKLLPVLTPDARDLVKPPFKBNPSQRI 326
DB 282 CLGAVLYEMLYGLPPFYSRNTAEMYNILAKPLQI-KNITNSAKHLBGLQOKRTKRL- 339
QY 327 GSGFGADAVQRRHPPFRHNMWDLAMRVDPFRPCLOSSEDDVSQDTRFTROTVD--- 382
DB 340 GAKDDEWEIKSHIFFSLINWDDLINKKITPPFPNPNVSGPSDLRHFDPFEETEE-PVPSISIG 398
QY 383 -SPDD---TALSASNAQFLGFTYVAPSVYDS 410
DB 399 RSPDSILVTASVKAEAELFGFSYAPP--WDS 428

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Wed Jul 7 12:18:44 2004

us-09-762-258-2.ra1

Page 9

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GenCore version: 5.1.6
(c) 1993 - 2004 Compu

using sw model

4, 08:42:56 ; Search time 146 Seconds

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B-1

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2
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Chosen parameters: 1365418

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45 Summary

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SUMMARIES

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US-09-430-564-1	Sequence 1, Appl1
US-08-966-316-10	Sequence 10, Appl
US-08-749-902-4	Sequence 4, Appl1
US-09-016-430-116	Sequence 126, Appl
US-09-016-434-118	Sequence 118, Appl
US-09-817-131-0	Sequence 1, Appl1
US-09-417-197-10	Sequence 70, Appl
US-09-417-197-118	Sequence 138, Appl
US-09-212-177-11	Sequence 1, Appl1
US-09-091-050-1	Sequence 1, Appl1
US-09-021-665-1106	Sequence 1206, Appl
US-09-256-465-1	Sequence 1, Appl1
US-09-167-322-3	Sequence 3, Appl
US-09-023-655-1004	Sequence 1004, Appl
US-09-621-982-18308	Sequence 18308, Appl
PCT-US95-08285	Sequence 8, Appl1
US-09-554-726A-11	Sequence 11, Appl1
US-09-554-726A-70	Sequence 20, Appl
US-09-417-1797-68	Sequence 68, Appl
US-09-394-455-39	Sequence 39, Appl1
US-09-394-455-3	Sequence 3, Appl1
US-09-467-082-3	Sequence 3, Appl1
US-09-394-455-5	Sequence 5, Appl1
US-09-394-455-35	Sequence 35, Appl1
US-08-685-852-1	Sequence 1, Appl1
US-09-016-434-1453	Sequence 1433, Appl
US-09-772-647-3	Sequence 3, Appl1

Alignments

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GenCore version 5.1.6
(c) 1993 - 2004 CompuGen Ltd.

using sw model

#4, 08:42:56 ; Search time 146 Seconds
(without alignments)
6902.677 Million cell updates/sec

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Gapext 1.0
277475446 residues

Chosen parameters: 1365418

00000
h 0%
t 100%
t 45 summaries

its NA:*
tdata/2/ina/5A.COMB.seq:*
tdata/2/ina/5B.COMB.seq:*
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equal to the score of the result being printed,
ists of the total score distribution.

SUMMARIES

DB ID Description
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US-09-430-564-1 Sequence 1, Appl1
US-08-966-316-10 Sequence 10, Appl1
US-08-749-902-4 Sequence 4, Appl1
US-09-016-434-126 Sequence 126, App
US-09-016-434-118 Sequence 118, App
US-08-817-310-1 Sequence 1, Appl1
US-09-417-197-70 Sequence 70, Appl1
US-09-417-197-138 Sequence 138, App
US-09-212-771-1 Sequence 1, Appl1
US-09-091-058-1 Sequence 1, Appl1
US-09-023-655-1205 Sequence 1205, Ap
US-08-256-445-1 Sequence 1, Appl1
US-09-167-322-3 Sequence 3, Appl1
US-09-023-655-1004 Sequence 1004, Ap
US-09-621-976-18308 Sequence 18308, A
PCT-US95-08295-8 Sequence 8, Appl1
US-09-554-726A-11 Sequence 11, Appl1
US-09-554-726A-20 Sequence 20, Appl1
US-09-417-197-68 Sequence 68, Appl1
US-08-394-455-39 Sequence 39, Appl1
US-09-394-455-3 Sequence 3, Appl1
US-09-467-082-3 Sequence 3, Appl1
US-09-394-455-35 Sequence 5, Appl1
US-08-685-852-1 Sequence 35, Appl1
US-09-016-434-1433 Sequence 1, Appl1
US-09-016-434-1433 Sequence 1433, Ap
US-09-772-647-3 Sequence 3, Appl1

RESULT 1
US-09-430-564-1
; Sequence 1, Application US/09430564
; Patent No. 6372467
; GENERAL INFORMATION:
; APPLICANT: John Blenis
; APPLICANT: Kay K. Lee-Fruman
; APPLICANT: Calvin J. Kuo
; TITLE OF INVENTION: P5456K AND P8556K GENES, PROTEINS,
; FILE REFERENCES: 00246/506002
; CURRENT APPLICATION NUMBER: US/09/430,564
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1998-10-25
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-430-564-1

Query Match 94.9%; Score 1724; DB 4; Length 1732;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1724; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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9 CCACGCGCCCGCGGCGCGCGCCGCGCCATGCGCGCGGTTGATTGGATTGGAGCG 68

149 GAGGAGGCGAGCGAGGCGGAGGCGGAGGCGAGGAGCTCAGCCCGCGGAGCGATGCCCTT 208
69 GAGGAGGCGAGCGAGGCGGAGGCGGAGGCGAGGAGCTCAGCCCGCGGAGCGATGCCCTT 128

209 GCGAGTTGAGGCGAGCTGGCTTGAAGCTTGCGAGCACTATGAAGAGTGAAGTGAAGT 268
129 GCGAGTTGAGGCGAGCTGGCTTGAAGCTTGCGAGCACTATGAAGAGTGAAGTGAAGT 188

269 GAGACCAAGCGAGAGCTTGCGCGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGG 328
189 GAGACCAAGCGAGAGCTTGCGCGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGGCGAGG 248

329 GTGCTGGCGCAAGCGGCGCTATGGAGAGGTGTTCCAGGTGCGCAAGGTGCGCAAGCGAC 388
249 GTGCTGGCGCAAGCGGCGCTATGGAGAGGTGTTCCAGGTGCGCAAGGTGCGCAAGCGAC 308

389 TTGGCGCAAAATATATGCTATGAAGCTCTTAAGAGAGCGCAAAATTTGCGCAATGCCAAG 448
309 TTGGCGCAAAATATATGCTATGAAGCTCTTAAGAGAGCGCAAAATTTGCGCAATGCCAAG 368

ALIGNMENTS

US-09-430-564-1
28 200.2 11.0 1619 4 US-09-394-455-14 Sequence 14, Appl1
29 198.6 10.9 2311 2 US-08-712-709-6 Sequence 6, Appl1
30 198.6 10.9 2311 3 US-09-111-444-6 Sequence 6, Appl1
31 198.6 10.9 2311 3 US-09-541-228-6 Sequence 772, App
32 198.6 10.9 2311 4 US-09-016-434-772 Sequence 1, Appl1
33 197 10.8 2370 4 US-09-031-295-1 Patent No. 5266464
34 195.6 10.8 2599 6 5266464-1
35 193.6 10.7 2104 4 US-09-113-930-1 Sequence 1, Appl1
36 168 9.3 2146 4 US-09-023-655-1191 Sequence 1191, Ap
37 166.4 10.3 3321 4 US-09-023-655-1361 Sequence 1361, Ap
38 184 10.1 2751 4 US-09-417-197-72 Sequence 72, Appl1
39 173.8 9.6 2754 3 US-09-429-322-3 Sequence 3, Appl1
40 169 9.3 2245 4 US-09-225-749-24 Sequence 24, Appl1
41 168 9.3 2146 4 US-09-842-307-1 Sequence 1, Appl1
42 168 9.3 2146 4 US-09-023-655-1362 Sequence 1362, Ap
43 168 9.2 1276 4 US-09-566-921-52 Sequence 52, Appl1
44 166.8 9.2 1276 1 US-07-688-352C-25 Sequence 25, Appl1
45 166.8 9.2 1276 5 PCT-US91-02714-24 Sequence 24, Appl1

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Db      988  CCCAGATGCCCCGAGACCTTGTCTCAAAAAGTTTCGAAACGGAATCCAGCCAGCGGATG 1047
Qy      1054  GGGTGGCCCAAGGGATGCTGCTGATGTCAGAGACATCCCTTTTTCGGCACTGAATTG 1113
Db      1048  GGGTGGCCCAAGGGATGCTGCTGATGTCAGAGACATCCCTTTTTCGGCACTGAATTG 1107
Qy      1114  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1173
Db      1108  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1167
Qy      1174  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1233
Db      1168  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1227
Qy      1234  CACAGCCCTCAGGAGAGTCACCAAGGCTTCTGAGGCTTCACTAGTCAGTCGCGCTC 1293
Db      1228  CACAGCCCTCAGGAGAGTCACCAAGGCTTCTGAGGCTTCACTAGTCAGTCGCGCTC 1287
Qy      1294  TGTCTGAGAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGGCG 1353
Db      1288  TGTCTGAGAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGGCG 1347
Qy      1354  CCTCAACAGTAGCCCCCGGCTGCCCTCAAGCCCTCAAGTTCTCCCTTTTGAAGGCTT 1413
Db      1348  CCTCAACAGTAGCCCCCGGCTGCCCTCAAGCCCTCAAGTTCTCCCTTTTGAAGGCTT 1407
Qy      1414  TCGGCCCCAGCCCAAGCTGCTGCGAGGCCCAAGAGCTTACTTACTTCACTCTGCAAC 1473
Db      1408  TCGGCCCCAGCCCAAGCTGCTGCGAGGCCCAAGAGCTTACTTACTTCACTCTGCAAC 1467
Qy      1474  GCGCGCGCCCTCGACCAACGCGCCCTCTGCCATCCGCTCCCTCAAGGAGCAAGAGTC 1533
Db      1468  GCGCGCGCCCTCGACCAACGCGCCCTCTGCCATCCGCTCCCTCAAGGAGCAAGAGTC 1527
Qy      1534  CAAGAGGCGCTGCGGCTGCAAGGCGCTGAGAGGCTGCGGCTGAGAGGTAAGCTT 1593
Db      1528  CAAGAGGCGCTGCGGCTGCAAGGCGCTGAGAGGCTGCGGCTGAGAGGTAAGCTT 1586
Qy      1594  GAGCCCTGTCCCTGCGGCTGT 1614
Db      1587  GAGCCCTGTCCCTGCGGCTGT 1607

```

RESULT 4
 US-09-016-434-125
 Sequence 126, Application US/09016434
 Patent No. 6500938
 GENERAL INFORMATION:
 APPLICANT: Janice Au-Young
 APPLICANT: Jeffrey J. Sellhamer
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
 TYPE OF INVENTION: PATHWAY GENE EXPRESSION
 NUMBER OF SEQUENCES: 1490
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 STREET: 3174 PORTER DRIVE
 CITY: PALO ALTO
 STATE: CALIFORNIA
 COUNTRY: USA
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016,434
 FILING DATE: HERewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:

```

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 126:
SEQUENCE CHARACTERISTICS:
LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: COLINFET02
CLONE: 1309709
US-09-016-434-126

Query Match      39.6%; Score 720; DB 4; Length 1607;
Best Local Similarity 99.1%; Pct. 3.7e-159;
Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

874  GAGCCTGGGCGCCCTGATGTAAGATGTCAGATGTCAGATGTCGCGCCCTTTACCGAGAGA 933
868  GCGGCTGGGAGCCGCTGATGTAAGATGTCAGATGTCAGATGTCGCGCCCTTTACCGAGAGA 927

934  CCGGAGAAACCATGATTAAGATCATAGGCGCAAGCTGGCATGCCCCCTTACTCTAC 993
928  CCGGAGAAACCATGATTAAGATCATAGGCGCAAGCTGGCATGCCCCCTTACTCTAC 987

994  CCGGAGAAACCATGATTAAGATCATAGGCGCAAGCTGGCATGCCCCCTTACTCTAC 1053
988  CCGGAGAAACCATGATTAAGATCATAGGCGCAAGCTGGCATGCCCCCTTACTCTAC 1047

1054  GGGTGGCCCAAGGGATGCTGATGTCAGAGACATCCCTTTTTCGGCACTGAATTG 1113
1048  GGGTGGCCCAAGGGATGCTGATGTCAGAGACATCCCTTTTTCGGCACTGAATTG 1107

1114  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1173
1108  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1167

988  CCGGAGAAACCATGATTAAGATCATAGGCGCAAGCTGGCATGCCCCCTTACTCTAC 1053
984  CCGGAGAAACCATGATTAAGATCATAGGCGCAAGCTGGCATGCCCCCTTACTCTAC 1047

1054  GGGTGGCCCAAGGGATGCTGATGTCAGAGACATCCCTTTTTCGGCACTGAATTG 1113
1048  GGGTGGCCCAAGGGATGCTGATGTCAGAGACATCCCTTTTTCGGCACTGAATTG 1107

1114  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1173
1108  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1167

1174  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1233
1168  GAGAGACTTCTGCGCTGCGGTGGAACCCCTTTCAAGCCCTGTCTGAGTCAGAGGA 1227

1234  CACAGCCCTCAGGAGAGTCACCAAGGCTTCTGAGGCTTCACTAGTCAGTCGCGCTC 1293
1228  CACAGCCCTCAGGAGAGTCACCAAGGCTTCTGAGGCTTCACTAGTCAGTCGCGCTC 1287

1294  TGTCTGAGAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGGCG 1353
1288  TGTCTGAGAGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCGTCAACCCAGGCG 1347

1354  CTTCAACAGTAGCCCCCGGCTGCCCTCAAGCCCTCAAGTTCTCCCTTTTGAAGGCTT 1413
1348  CTTCAACAGTAGCCCCCGGCTGCCCTCAAGCCCTCAAGTTCTCCCTTTTGAAGGCTT 1407

1408  TCGGCCCCAGCCCAAGCTGCTGCGAGGCCCAAGAGCTTACTTACTTCACTCTGCAAC 1467
1414  TCGGCCCCAGCCCAAGCTGCTGCGAGGCCCAAGAGCTTACTTACTTCACTCTGCAAC 1473

1474  GCGCGCGCCCTCGACCAACGCGCCCTCTGCCATCCGCTCCCTCAAGGAGCAAGAGTC 1533
1468  GCGCGCGCCCTCGACCAACGCGCCCTCTGCCATCCGCTCCCTCAAGGAGCAAGAGTC 1527

1534  CAAGAGGCGCTGCGGCTGCAAGGCGCTGAGAGGCTGCGGCTGAGAGGTAAGCTT 1593
1528  CAAGAGGCGCTGCGGCTGCAAGGCGCTGAGAGGCTGCGGCTGAGAGGTAAGCTT 1586

1594  GAGCCCTGTCCCTGCGGCTGT 1614

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QY	501	CCCTTATGTGGAACCTGCGCTATGCGCTTCCAGACCTGGGAGCAAACTTACCTCATCTTG	560
Db	889	CTTCTATGTGGAAGCTTATGCTTTATGCTTCCAGACGAGGAAACTATACCTTATCTTG	948
QY	561	AGTGGCTCAGTGTGGCGAGCTCTTCAACGATCTGGACCGAGAGGGCACTTCTCGAAG	620
Db	949	AATATCTCAGGGGTGGAGAGCTGTCTCAGTCATTTGGACCGCTGAGGGCACTCTTCTTGAAG	1008
QY	621	ATAGCGCGTGTCTTACCTGGCTGATCAGGCTGTGGCTGTGGGCACTGTCCATCCAG	680
Db	1009	ATACCACTGCTTCTTATCTTAAAGCAATATTTTGGCTTGGGCACTTACCAAACTGG	1068
-QY	681	GCATCATCTACCGGAGCTTCAAGCCGAGAAATCATCTGCTCAGACGCAAGGCGCACTCA	740
Db	1069	GCATCATCTACCGGAGCTTCAAGCCGAGAAATCATCTGCTCAGATGCAAGGAGCATGGA	1128
QY	741	AACTGACCGCATTTTGGATCTTGGCAAGAGCTTATTCATGAGAGGCGCGCTCATCACT	800
Db	1129	AGCTCACCGCATTTTGGATCTTGGCAAGAGCACTATCAAGAGGATTTGTCCACCACT	1188
QY	801	TCTGGCGGACCACTTGTAGTACATGGCGCTGTGAGATCTGTGGTGGCGAGTGGCAACCGG	860
Db	1189	TCTGGCGGACCACTTGTAGTACATGGCACTGTGAAATTTTATCCAGAACTGGCCATGGCAAG	1248
QY	861	CTGTGACTGTGTGAGCTCTGGGGGCGCTGTGATGTACGATCTCTCATGTGCGCGCT	920
Db	1249	CAGTGCATGTGTGTGCTCTGGGGGCGCTCTCATGTGTGATCATCTCTCAAGAGTCCACCT	1308
QY	921	TTAOCGACAGAACCGGAAAGAAACATGATTAAGATCATCAGGGCGCAAGCTGGCACTGC	980
Db	1309	TACCGCGGAGATGTGCAAGAGACCATGAGACCATTTGTGAAGCCAGCTCATCTGC	1368
QY	981	CCCCCTTACCTCAACCCAGATGCCCGGGACTTGTGTCAAAAAGTTTGTGAACGGAATCCA	1040
Db	1369	CAGCTTACCTCAACCCAGAGGAGGATCTGTGTGCTGTGCTGTGAGAGGAGGAGAGAC	1428
QY	1041	GCGAGCGATTTGGGGGTGGCCCAAGGAGTGTGTCTGATGTGCAAGAGACATCCCTTTTCC	1100
Db	1429	CTCAGCGCTTTGGCAAGGAGCCGAGAGATGGCGGCGCTGTTCAAATACCCCATTTCTCA	1488
QY	1101	GGCACAATATTGGGACGACCTTCTGGGCTGTGGCTGTGACCCCTTTTCAAGGCGCTTTC	1160
Db	1489	AACAGCTGACCTGGGACGATGTGTCTGCGCAGACGCTTGGACCGCTTATAAACCGCTCT	1548
QY	1161	TGCAGTCAAGAGAGACGTGAGCCGATTGATCCCGCTTCAACAGCGCAGACGCCGCTGG	1220
Db	1549	TGAGAGCGAGAGATATGTCTCAAGTTGTGATACAAAGTTTCAAGAAATTTCCAGTGG	1608
QY	1221	ACAGTCTGATGACACAGCCCTCAGCGAGAGTGGCAACAGGCGCTTCTGGGCTTCACAT	1280
Db	1609	ATTCCCTGTGATGATCAACGCTTACGCGAAAGTGCCTAATTTATTTTCCAAAGTTTCACT	1668
QY	1281	ACGTGGCGCGCTGTGTCTGTGACAGCATCAAGAGGGG	1318
Db	1669	ACGTGACACCTCGATCTGTGAGAGATATGATCGGGC	1706

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PKB-EGFP fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (2178)
US-09-417-197-70

```

Query Match	14.4%	Score 260.8;	DB 4;	Length 2181;
Best Local Similarity	57.0%	Pred. No. 1e-51;		
Matches 517;	Conservative 0;	Mismatches 384;	Indels 6;	Gaps 2

QY	343	GGGCTATGCAAGGATGTTTCACAGGTGCGCAAAAGTGCACAAAGGCACCAACTGCGCAAAATATA	402
Db	468	GGGCAAGGCGCACTTTCGGCAAGGTGATTCCTGTGTGAGAGAGAGAGGCACAGGCGGCTACTA	527
QY	403	TGCGATGAAAGTCCTTAAGAAAGGCGCAAAATTTGTGCGCATGTCCCAAGGACACAGCAAC	462
Db	528	CGCATGAAAGATCCTCAAGAAAGAAAGTCACTGTGTGGCCAAAGGACCAAGG--TGCGCCACAC	584
QY	463	ACGGGCTAGGCGGAACATTTAGAGTCAGTGAACACCCCTTTATTGTGGAACATGCGCTTA	522
Db	585	ACTCACCGAAGAACCGCGTCTCGAGAACTCCAGGCAACCCCTTCTCAACGCGCTGAAGTA	644
QY	523	TGCGTTCCAGACTGTGTGCAAACTTACCTCATCTTGAATGCTCACTGTGTGGCGAGCT	582
Db	645	CTCTTTCCAGACCCACAGACCGGCTCTCTGTGTATGAGAGTACCCCAACGGAGGGCGAGCT	704
QY	583	CTTCAAGCATTTGAGAGGAGAGGAGGCACTTTCCTGGAAGATACGGGCTGTCTTCACTGAGC	642
Db	705	GTTTTCACACTGTCCCGGAAAGCTGTGTCTCCGAGGACCGGGCCCGCTTCTATAGGCGC	764
QY	643	TGAGATCAAGCTGGCCCTTGAGCCATCTCCACTC--CGAGGCATCATTAACGGAGACT	699
Db	765	TGAGATGTGTCAAGCCCTGAGACTCTCGACTCGAGAAAGAACGTGTGTACCGGAGACT	824
QY	700	CAAGCCCGAAGAACTATGCTCTACAGACCCAGGGCCACATCAACTGACCCGACTTTGACT	759
Db	825	CAAGCTGAGAACTCACTATCTGACAAAGAGAGGGGCACTTAAAGATCAAGACTTGGGCT	884
QY	760	CTGCAGAGAGCTATTCATGAGAGGCGGCGCTCATCACACTTCTGCGGCACATTTAGTA	819
Db	885	GTGCAGAGAGGAGATCAAGAGCGGTGCACCATGAGACCTTTTGCGGCAACCTGAGTA	944
QY	820	CATGAGCCCTTGAGATTCTGTGTGCCAATGTGCGCAAAACCGGCTGTGATCTGTGTGAGCT	879
Db	945	CTGTGCCCCGAGGTGTGTGAGAGCAATGACTAAGGCGGTGACATGTGACTGTGTGGGCT	1004
QY	880	GGGGGCGCTGATGTAGACACATGCTCACTGTGATCCGCGCCCTTTACCGGAGAAACCGAA	939
Db	1005	GGGCGTGTGATGTACAGATGATGTGTGGGTGGCTGTGCCCTTTCAAAACAGGACATAGA	1064
QY	940	GAAGAACATGATTAAGATCATCAGGGGCAAGCTGGCACTGCCCCCTTACCTCACCCCGAA	999
Db	1065	GAAGCTTTTGTAGCTCAATCCATGAGAGAGATCGGCTTCCGGGCAACGCTGTGTTCCGA	1124
QY	1000	TGCGCGGAGACTTGTCAAAAGTTTCAAGAACGAAATCCAGCGAGCGAGTATGGGCGGTGG	1059
Db	1125	GGCGCAAGTCTTGTCTTCAAGGCTGCTTCAGAGAGAACCCCAAGAGAGGCTTGGGCGGGG	1184
QY	1060	CCGAGGGAGATGCTGCTGATGTGCAGAGACATCCCTTTTTCGGGCAATGAATTGGAGGA	1119
Db	1185	CTCCGAGGAGCGCAAGAGAGATCATGACAGCATCGCTTTTTCGCGGTATCGTGTGGACGA	1244
QY	1120	CGTTCTGTGCGCTGTGTGTGAGACCCCGCTTTCAGGCGCGTGTGTGAGAGTCAAGAGAGAGT	1179
Db	1245	CGTGTACGAGAGAGAGCTCAGGCCACCTTTCAGGCGCCAGGTCAAGCTTCGAGAGACTGACAC	1304
QY	1180	GAGCCAGTGTATGATCCGCTTTCACACGGGCAAGCGCGGTGACAGTCTTATGTACACAC	1239
Db	1305	CAGGTATTTTGTATGAGAGGTTCAAGGCGCCAGATGATCAATCAACCAACTGTGACCAAGA	1364
QY	1240	CTTCAGC 1246	

Db 1365 TGAAGC 1371

|||||

RESULT 8
US-09-417-197-138
; Sequence 138; Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
; APPLICANT: Ole Thastrup, et al.
; TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An
; FILE REFERENCE: 3759-0110P
; CURRENT APPLICATION NUMBER: US/09/417,197
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PKB fusion
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138

Query Match 14.4%; Score 260.8; DB 4; Length 2184;
Best Local Similarity 57.0%; Pred. No. 1e-51;
Matches 517; Conservative 0; Mismatches 384; Indels 6; Gaps 2;

QY 343 GGGCTATGCGAAGGTGTTCCAGGTGCGAAGGCGCAAGGACCAACTTGGGCAAAATATA 402
Db 1209 GGGCAAGGGGCACTTCCGCAAGGATGATCTGTGAGAGAGAGCCACAGCCGCTACTA 1268
QY 403 TGCATGAAGATCTTAAGAAAGGCAAAATGTGCGCAATGCCAAGACAAGACACAC 462
Db 1269 CGCATGAAATCTCTCAAGAAAGATCATGTGCGCAAGAGG---TGCCCAACAC 1325
QY 463 ACGGCTGAGCGGCAACTTTAGATGAGAGAGACCCCTTATTTGTGAATGTGCGCTA 522
Db 1326 ACTGACCGAAGACCGGCTCTGCGAAGATCTGAGGACCCCTCTCAACACCTGAAATA 1385
QY 523 TGCCTTCAGACTGTGCGCAAACTCTACTCATCTTGAATGCTCAAGTGTGCGAGCT 582
Db 1386 CTCTTTCAGACCCAGACCGGCTCTGCTTGTGATGAGATGAGCCAGCGGGCGAGCT 1445
QY 583 CTTCAGCATCTGAGAGCGAAGGCGCATCTTCTGAAAGATAGCGGCTGCTTTACTGCG 642
Db 1446 GTTCTTCCACCTGTCCCGGAGAGGTGTGTTCTCCGAGAGCCGGGCGCTTATGAGCG 1505
QY 643 TGAATCAAGCTGGGCTTGGGCACTCTCACTC---CAAGGCAATCATACCGGGACCT 699
Db 1506 TGAATGTGTCAAGCTTGAACCTGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1565
QY 700 CAAGCCGAGAGACATCATGCTCAAGCGACGAGGCGCATCAATCAACTGACCGACTT 759
Db 1566 CAAGCTGAGAGACCTCATGCTGAGCAAGAGAGCGGCGCATTAAGATCAAGACTT 1625
QY 760 CTGCAAGAGATCTATTCATGAGAGAGGCGCGTCACTCAACCTTGGGCGACCAATTAGTA 819
Db 1626 GTTCAG 1685
QY 820 CATGCGCCCTGAGATTCTGTGCGCAGTGGCCAAACCGGCGTGTGAGCTGTGAGCGCT 879
Db 1686 CCTGCGCCCGAGAGGTGTGAGAGACAATGACTACGCGCGGTGAGTGAATGAGGAGGCT 1745
QY 880 GGGGCGCTGATGATGAG 939
Db 1746 GGGGAGGTGATGATGAG 1805
QY 940 GAAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999

Db 1806 GAACTTTTGAAGCTATCTCTCAAGAGAGATCCCTTCCCGGCAAGCTTGTGCTCGA 1865

|||||

RESULT 9
US-09-212-771-1
; Sequence 1; Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF ART-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Query Match 14.4%; Score 260.8; DB 2; Length 2610;
Best Local Similarity 57.0%; Pred. No. 1.1e-51;
Matches 517; Conservative 0; Mismatches 384; Indels 6; Gaps 2;

QY 343 GGGCTATGCGAAGGTGTTCCAGGTGCGAAGGCGCAAGGACCAACTTGGGCAAAATATA 402
Db 666 GGGCAAGGGCACTTTCGGCAAGGTATCTGTGAAAGAGAGAGGCGCAGGCGTACTA 725
QY 403 TGCATGAAGATCTTAAGAAAGGCAAAATTTGTGCGCAATGCCAAGAGACAGACACAC 462
Db 726 GCGCATGAAGATCTTAAGAAAGAGTCAATGTCGCGCAAGAGAGAG---TGGCCACAC 782
QY 463 ACGGCTGAGCGGAACTTCTAGATGAGTGAAGAGACCCCTTATTTGTGGAATGAGCTA 522
Db 783 ACTCAACGAGAGACGGGTCTGAGAGATCTCCAGAGACCCCTTCTCAAGCGCTGAAATA 842
QY 523 TGCCTTCAGACTGTGCGAACTCTACTATCTTGAATGCTCAAGTGTGAGGAGCT 582
Db 843 CTCTTTCAGACCCAGACCGGCTCTGCTTGTGATGAGAGTACGCGCAAGGCGGAGCT 902
QY 583 CTTCAGCATCTGAG 642
Db 903 GTTCTTCAACCTGTCTCCGGAAGAGTGTGTCTTCCAGAGACCGGCGCTTATAGGCGC 962
QY 643 TGAATCAAGCTGAGCGCTTGGGCACTCTCACTC---CAAGGCAATCATCTACCGGACCT 699
Db 963 TGAATGTGTGAGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1022

NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HEREMITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1206:
SEQUENCE CHARACTERISTICS:
LENGTH: 2610 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g190827
US-09-023-655-1206

Query Match 14.4%; Score 260.8; DB 4; Length 2610;
Best Local Similarity 57.0%; Pred. No. 1,1e-51;
Matches 517; Conservative 0; Mismatches 384; Indels 6; Gaps 2;

QY 343 GGGCTATGCGAAGTGTTCAGGTGCGAAGGTCGACCAACTTGGGCAAAATATA 402
DB 666 GGGCAAGGCACTTCGCGAAGGTGATCTGTGAGAGAGAGGCGCACAGCGCTACTA 725
QY 403 TGCATGAAGTCTCTAGAGAGGCGCAAAATTTGGCGAATGCCAGACACAGACAC 462
DB 726 CGCATGAGATCTCTAGAGAGGAGTCACTGTGGCCAGAGAGAGG--TGCCCAAC 782
QY 463 ACGGCGTGAAGCGGAACTTCTAGAGTCAAGCAACCCCTTATTTGTGAACTGGCCTA 522
DB 783 ACTCACCGAGAACCGGCTCTGCGAAGCTCAGGACCCCTTCTCAACCCCTGAGTA 842
QY 523 TGCCTTCAGACGTGTGGGCAACTCTACCTCACTCTTGAATGCTCAATGTGGGCAAGCT 582
DB 843 CTCTTTCAGACCCAGACCGCTCTGTCTTTGTATGAGATAGCCAAACGCGGCGAGCT 902
QY 583 CTTCACGATCTGAGAGAGAGGAGCTCTTCTGAGAGATACGGCTGTCTTACTTGGC 642
DB 903 GTTCTTCACTCTTCCCGGAGAGGTGTCTCCGAGAGCCGGCCCGCTTCTATGGCCG 962
QY 643 TGAATACGCTGGCCCTGGGCACTTCACTC---CGAGGCACTACTTACCGGAGCT 699
DB 963 TGAATGTGTGACCGCTGACTTACTGCACTCGAGAGAGAGTGTGTACCGGAGCT 1022
QY 700 CAAGCCGAGAGATCATGCTCAGACGCGGCGCACTCAATCAACGACCTTTGAACT 759
DB 1023 CAAGCTGGAGAACTCATGCTGAGACAGAGAGGCGCACTTATGATCAAGACTTGGGCT 1082
QY 760 CTGCAAGAGTCTATTCAGAGAGGCGCGCTCACTCAACCTTCTGCGGAGCACTTGA 819

DB 1083 GTGCAAGAGAGGATCAAGACGCTGCCACCATGAAACCTTTTGGCGACACTGACTA 1142
QY 820 CATGGCCCTTGAGATTCTGTGCGAGTGGCCACACCGGCTGTGATCTGTGAGAGCT 879
DB 1143 CTGGCCCGGAGGTCTGAGAGGACATGACTACAGCCGCTGTGATGAGCTGTGGGCT 1202
QY 880 GGGGCGCTGATGATGAGACATGCTCACTGATGCGCGCCCTTTACCGGAGAGACGGAA 939
DB 1203 GGGCGTGTATGATGAGAGATGATGCGGTGCGCTGCTCTTCAACAGAGACATGA 1262
QY 940 GAAACCATGATTAATGATCATCAGGGCAAGTGGCACTGCGCCCTTACCTCACTCCAG 999
DB 1263 GAAGCTTTTGAAGTACTCTTCAAGAGAGATCCGCTTCCGCGACGCTGTCCCGA 1322
QY 1000 TCGCCGAGACCTTGTCAAAAAGTTTGTAAACGAAATCCAGCCAGCGGATGGGGGTG 1059
DB 1323 GGGCAAGTCTTCTTCAAGGGCTGTCAAGAGAGACCCAGAGAGAGCTTGGCGGAG 1382
QY 1060 CCAGAGGATGCTGTGATGTCAGAGAGATCCCTTTTTCGCGACATGAATTGGAGCA 1119
DB 1383 CTCCGAGAGCCAGAGAGATCATGAGCATGCTCTTGTCCGATTCGTGTGGAGCA 1442
QY 1120 CTTCTGGCGTGGCGGTGAGACCCCTTTCAGGCTGTCTGCAATGACAGAGAGAGCT 1179
DB 1443 CGTGTACGAGAGAGAGCTCAGCCACCTTCAAGCCCAAGTACAGCTGAGACTGAC 1502
QY 1180 GAGCCAGTTGATATCCCGCTTCAAGGACAGAGCGCGGTGAGATGCTGATGACAGC 1239
DB 1503 CAGGATTTTGAAGAGAGTTCAGGCGCCAGATGATCAACATCAACCACTGACCAAG 1562
QY 1240 CCTCAGC 1246
DB 1563 TACAGC 1569

RESULT 12
US-09-256-465-1
; Sequence 1, Application US/09256465
; Patent No. 6043090
; GENERAL INFORMATION:
; APPLICANT: Bect P. Monia
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION
; FILE REFERENCE: RTS-0035
; CURRENT APPLICATION NUMBER: US/09/256,465
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (88)..(1533)
US-09-256-465-1

Query Match 14.0%; Score 253.8; DB 3; Length 1599;
Best Local Similarity 54.0%; Pred. No. 4,1e-50;
Matches 569; Conservative 0; Mismatches 472; Indels 12; Gaps 2;

QY 313 CTTTGAAGTGTGCGGTGTGGGAGAGGGGCTATGGCAAGGTGTCAGGTGAGAA 372
DB 540 CTTTGAAGTGTGCGGTGTGGGAGAGGGGCTATGGCAAGGTGTCAGGTGAGAA 599
QY 373 GGTGCAAGGCAACCTTGGGCAAAATATATGCAATGAAGTCTTAAAGAGAGCCAAAT 432
DB 600 G-----AAGGCACTGGCCGCTTACTAGCCATGAAGATCTGCGAAAGAGAGTAT 650
QY 433 TGTGGCAATGTCAGAGACAGACACAGAGGCTTAAAGGCAATCTTGAAGTCACT 492
DB 651 CATTCGCAAGG---ATGAAGTGTCTCAGACAGTCAAGAGAGCCGCGGTCTTCAAGAAC 707
QY 493 GAAGCAACCCCTTATTTGTGAACTGAGCTATGCTTCAAGACTGTGGCAACTTACT 552

1068 TGGCCGGGCGCTGAGCTGTGGGGCTGGGTGTGATGTACAGATGATGTGGCGCC 1127
QY 913 GCCCGCTTTTCCCGAGAAACCGAGAAACCATGTGATTAATCATCGAGGCAAGCT 972
Db 1128 CCGCCCTTCTACACACGAGACGAGCGCTCTTGGAGCTCATCTCTATGGAAGAT 1187
QY 973 GGCACGTGCGCCCTTACCTACCCCAAGATGCGGGGACCTTGTCAAAAAGTTTGAAGC 1032
Db 1188 CCGCTTCCCGGCGACGCTCAGCCCGGAGCAATCTCTGTGCTGGCGCTCTTAAGAA 1247
QY 1033 GAATCCAGCCAGCGGATGGGGGTGGCCCAAGGATGTGTGTATGTGACAGACATCC 1092
Db 1248 GGACCCCAAGCAGAGCTGTGGTGGGGGCGCCAGAGATCCAGAGAGGTATGAGCAG 1307
QY 1093 CTTTTCGCGGACATGATGGAGAGACCTTCTGGCGGTGAGTGTGAGACCCCGCTTGA 1152
Db 1308 GTTCTTCTCAGCATCACTGACGAGAGGTGTGCAAGAAAGCTCTGCAACCTTCA 1367
QY 1153 GCCCTGTCTGAGTCAAGAGAGAGAGTGAAGCAGTTGATACCGCTTCAACAGGCAAG 1212
Db 1368 ACCTGAGTCAAGTCCAGAGTCAAGAGTCAAGTCAATTTGATGATGAATTAACCGCCAGTC 1427
QY 1213 GCCGTGAGACATCTTATGACACAGCCCTTACGAGAGTCCCAACAGGCTTCTGGG 1272
Db 1428 CATCAATACACACCCCTGACCGCTATGACAGCTGGGCTTACTGAGCTGAGCAGCG 1487
QY 1273 CTTACATATGAGGCGCGCTGTGTGCTGACAGATCAAGAGGCTTCTTCCAGCC 1332
Db 1488 GACCCACTTCCCGAGTTCCTTCTACTGCGCCAGATCCGGAATGAGAGTGTGCCAGC 1547
QY 1333 CAAGCTGCGCTCAACCCAGGCGCTCAACAGTAG 1365
Db 1548 CAGAGAGCAGCGCTGCTGCTCATCAACCGCTGG 1580

RESULT 14
US-09-023-655-1004
Sequence 1004, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1004:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g178325
US-09-023-655-1004

Query Match 14.0%; Score 253.8; DB 4; Length 1599;
Best Local Similarity 54.0%; Pred. No. 4, 1e-50;
Matches 569; Conservative 0; Mismatches 472; Indels 12; Gaps 2;

QY 313 CTTTGAAGCTGCTGCGTGTGCTGAGCAAGGGGCTATGCGAAGTGTTCAGGTGGA 372
Db 540 CTTGACATATCTCAACCTCTTGGCAAGGAACTTTGGCAAGTATCTGTGCGGGA 599
QY 373 GGTGCAAGGCAACCACTTGGGCAAAATATATGCAATGAAGTCTTAAGAGCCAAAT 432
Db 600 G-----AAGCCACTGGCCGCTACTAGCATGAAGATCTGCAAGAGAGTCAAT 650
QY 433 TGTGCGCAATGCCAAGACACAGACACACAGGGCTGAGCGGAACTTTAGATCACT 492
Db 651 CATTCGCAAG--ATGAAGTGTCTACACAGATCAACCGAGAGCGGGCTCTCCAGAAC 707
QY 493 GAAGCACCCTTTATTTGGAATGCGCTTATGCTTTCAGACTGTGAGCAAACTTACT 552
Db 708 CAGGACCCGTTCTTCACTGCGCTGAGATGATCTTCCAGACCAACGACCGCTGTGCT 767
QY 553 CAGCTGAGTCTCAGTGTGAGGAGGCTCTTCAAGCATGAGCATGAGAGAGAGGCACTT 612
Db 768 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 827
QY 613 CTTGAAATACGAGCTGCTTCTTACTGCTGATGATCAAGCTGAGCTGAGGCTGATCTCA 672
Db 828 CACAGAGAGAGCGGCGCGGCTTTATGTGACAGATGTGCTGGCTTGAATTTGCA 887
QY 673 CTTCCAGGAGCATCTTACCGGAGCTGAGCGCCAGAACTATGATGCTCAGAGCCAGG 732
Db 888 CTGGCGGAGCGTGTATACCGGACATGATGAGTGAAGAACTTATGATGAGCAAGATAG 947
QY 733 CCACATCAACTGACCGACTTGTGACTGTGCAAGAGTCTATCAATGAGGCGCGCTCAC 792
Db 948 CCAATCAAGATCACTGACTTTGGCTCTGCAAAAGGCAATCAATGACGGGCCACAT 1007
QY 793 TCACCTTTTGGCGGACCATGATGATGATGATGATGATGATGATGATGATGATGAT 852
Db 1008 GAAACCTTCTGTGAGACCCCGAGATACCTGCGCTTGAAGTCTGAGAGAGCAATGACT 1067
QY 853 CAACGGGCTGTGACTGTGAGAGCTGAGGAGCTGATGATGATGATGATGATGATGATG 912
Db 1068 TGGCCGGGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1127
QY 913 GCCCGCTTTTACCGGAGAAACCGAGAAACCATGTGATTAATCATCGAGGCAAGCT 972
Db 1128 CTTGCTTCTACACACGAGACGAGCGCTTCTTCAAGTCTCATCTCATGAGAGAT 1187
QY 973 GGCACGTGCGCCCTTACCTACCCCAAGATGCGGGGACCTTGTCAAAAAGTTTGAAGC 1032
Db 1188 CCGCTTCCCGGCGACGCTCAGCCCGGAGCAATCTCTGTGCTGGCGCTCTTAAGAA 1247
QY 1033 GAATCCAGCCAGCGGATGGGGGTGGCCCAAGGATGTGTGTATGTGACAGACATCC 1092
Db 1248 GGACCCCAAGCAGAGCTGTGGTGGGGGCGCCAGAGATCCAGAGAGGTATGAGCAG 1307
QY 1093 CTTTTCGCGGACATGATGGAGAGACCTTCTGGCGGTGAGTGTGAGACCCCGCTTGA 1152
Db 1308 GTTCTTCTCAGCATCACTGACGAGAGGTGTGCAAGAAAGCTCTGCAACCTTCA 1367
QY 1153 GCCCTGTCTGAGTCAAGAGAGAGAGTGAAGCAGTTGATACCGCTTCAACAGGCAAGC 1212

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Db 1368 ACCTCAGCTACCTCCAGGCTCGACACAGGTACTTTCGATGATGAAATTTCACGCCCAAGTTC 1427
QY 1213 GCCGGTGGACAGTCTTGATGACACAGCCCTCAGCGAGAGTGCACACAGGCTTTCCTGGG 1272
Db 1428 CATCAATACACACCCCTTACCGCTATGACAGCTGAGGCTTACGAGCTGACACAGG 1487
QY 1273 CTTCACTAGTGGGCGGCTGTGCTTCCCTGACAGCATCAAGAGGCTTTCCTTCCAGCC 1332
Db 1488 GACCCACTTCCCCCAAGTTCTTCTACTGCGCAGCATTCGCGAGTGAAGCACTTGCACAG 1547
QY 1333 CAAGCTGCGCTCACCAGCGGCTCTCAACAGTAG 1365
Db 1548 CAGAGGACGACCGCTGCTGCTGACATCAACCGCTGG 1580
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RESULT 15

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US-09-621-976-18308
; Sequence 18308, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 18308
; LENGTH: 503
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-621-976-18308
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Query Match 13.8%; Score 251.4; DB 4; Length 503;
Best Local Similarity 80.2%; Pred. No. 1e-49;
Matches 397; Conservative 1; Mismatches 2; Indels 95; Gaps 5;
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QY 572 GGTGGGAGCTCTTCAGCATCTGAGCGAGAGGAGCATCTTCTGGAAGATAAGGCTGC 631
Db 100 GGTGGGAGCTCTTCAGCATCTGAGCGAGAGGAGCATCTTCTGGAAGATAAGGCTGC 159
QY 632 TTCTACCTGCTGAGATCAAGCTGGGCTGGGCAATCTCCAGGCAATCACTTAC 691
Db 160 TTCTACCTGCTGAGATCAAGCTGGGCTGGGCAATCTCCAGGCAATCACTTAC 218
QY 692 CGGGACCTCAAGCGCGAAGCATCATGCTCAAGCGCAAGGCGCAATCAATCAACCGAG 751
Db 219 CGGGACCTCAAGCGCGAAGCATCATGCTCAAGCGCAAGGCGCAATCAATCAACCGAG 277
QY 752 TTGGAATCTGCAAGAGTCTATCATGAGGGGCGCGTCACTCAACCTTCTGCGGCAAC 811
Db 278 TTGGAATCTGCAAGAGTCTATCATGAGGGGCGCGTCACTCAACCTTCTGCGGCAAC 337
QY 812 ATTGATCAATGCGCCCTTGAGATTCTGTCGCGAGTGGCCACACCGGCTGTGACTGG 871
Db 338 ATTGATCAATGCGCCCTTGAGATTCTGTCGCGAGTGGCCACACCGGCTGTGACTGG 348
QY 872 TGGAGCTGGGGGCTCTGATGTACGACATGCTCACTGATCGCGGCTTTACCGGAGAG 931
Db 349 -----CGGCTTTACCGGAGAG 366
QY 932 AACCGAAGAAAACATGATTAAGATCATCAGGGGCAAGCTGCACTGCCCCCTTACTTC 991
Db 367 AACCGAAGAAAACATGATTAAGATCATCAGGGGCAAGCTGCACTG-CCCCCTTACTTC 425
QY 992 ACCCGAATGCCCGGAGCTTGTCAAAAAGTTTCTGAAAGGAAATCCAGCCAGGAGATT 1051
Db 426 ASCTCGATGCTCCGAGACTTGTCAAAAAG-TTCTGAAAGGAAATCCAGCCAGGAGATT 484
QY 1052 GGGGTTGGCCCAAGG 1066
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Db 485 GGGGTTGGCCCAAGG 499
Search completed: July 3, 2004, 10:10:31
Job time : 153 secs
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QY 25 GluGluGlySerGluGluGluGluProGluLeuSerProAlaAspAlaCysProLeu 44
 Db 69 GAGAGAGGAGCGAGGCGAGGCGAGAGCTCAGAGCCCGCGAGCGATCTCCCTT 128
 QY 45 AlaGluLeuArgAlaAlaGlyLeuGluProValGlyHISGlyGluGluValGluLeuThr 64
 Db 129 GCCAGATTGAGGCGAGCTGAGCTTGAAGCTCTGGGACACTATGAAGAGTGGAGCTGACT 188
 QY 65 GluThrSerValAsnValGlyProGluArgIleGlyProHISGlyPheGluLeuLeuArg 84
 Db 189 GAGACCGAGCTGAAAGTGGCCCGAGAGCGCATCGGCGCCCATGCTTGAAGCTGCTGCGT 248
 QY 85 ValLeuGlyGlyGlyGlyGlyGlyValPheGluValArgValArgValGluGlyThrArg 104
 Db 249 GTGCTGGGCAAGGGGGGCTATGGAGAGTGTCCAGGTGCAAGAGGTGCAAGGCAAC 308
 QY 105 LeuGlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLys 124
 Db 309 TTGGGCAAAATATATGCTCATGAAAGTCTTAAGGAGGCCAAATTTGGCCAAATGCGAAG 368
 QY 125 AsnThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHISProPheIle 144
 Db 369 GACACAGACACACACGCGGCTGAGCGGAACTTCAGAGCTGAGAGCAACCCCTTATT 428
 QY 145 ValGluLeuAlaTyrAlaPheGluThrGlyGlyLysLeuTyrLeuIleLeuGluCysLeu 164
 Db 429 GTGGAACTGGCTATGCTTCCAGACTGCTGGCAACTCTACTCATCTTGAGTGGCTTC 488
 QY 165 SerGlyGlyGluLeuPheThrHISLeuGluArgGluGlyIlePheLeuGluAspThrAla 184
 Db 489 AGTGTGGCGAGCTCTTCAAGCATCTTGAGCGAGAGGAGCATCTTCTCGAAGATACGGCC 548
 QY 185 CysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHISLeuHISSerGlnGlyIleIle 204
 Db 549 TGCTTCACTGCTGATGATCAAGCTGGCTGGCCATCTCCAGGAGCATCATC 608
 QY 205 TyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHISLysIleLysLeuThr 224
 Db 609 TACCGGAGCTCAAGCCCGAGAACATCATCTCAGAGCGAGCGCCCAATCAACTGAGC 668
 QY 225 AspPheGlyLeuGlyLysGlySerIleHISGlyValAlaThrHISThrPheCysGly 244
 Db 669 GACTTGGACTGCAAGAGAGTATTCATGAGAGGCGCCCTCATCAACATCTTCTCGGC 728
 QY 245 ThrIleGluTyrMetAlaProGluIleLeuValArgSerGlyHISAsnArgAlaValAsp 264
 Db 729 ACCATTGAGTACATGGCCCTTGAGATTCTGTGCGAGTGGCAACCGGGCTGTGGAGC 788
 QY 265 TrpTrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAla 284
 Db 789 TGGTGGAGCTCGGGGCGCTGATGTACGACATCTCATGAGCGCCCTTACCGCA 848
 QY 285 GluAsnArgLysLysThrMetLysLysIleIleArgGlyLysLeuAlaLeuProTyr 304
 Db 849 GAGAGCCGAGAGAAACATGATGATGATGATGAGAGAGAGTGGCACTGCGCCCTTAC 908
 QY 305 LeuThrProAspAlaArgAspLeuValLysPheLeuLysArgAsnProSerGlnArg 324
 Db 909 CTCACCCCAATGCTCCCGGAGCTGTCTCAAAAGTTTCTGAAAGGAGATCCACAGCCAGCG 968
 QY 325 IleGlyGlyGlyProGluAspAlaAlaAspValGluArgHISProPhePheArgHISMet 344
 Db 969 ATTGGGGGAGGCGCGAGAGTGTGATGATGATGATGAGAGATCTCTTTTCCGCGCAAG 1028
 QY 345 AsnTrpAspAspLeuAlaTyrArgValAspProPheArgProCysLeuGlnSer 364
 Db 1029 AATTGGGACGACCTTCTGGCTGGCGGTGAGACCCCTTTCAGGCGCTGTGCGAGTCA 1088
 QY 365 GluGluAspValSerGluPheAspThrArgPheThrArgIleThrProAlaAspSerPro 384
 Db 1089 GAGGAGGAGCGTGGAGCGAGTTGATACCGCTTCAACGAGGAGCGCGGTGAGCAATGCTCT 1148

QY 385 AspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAla 404
 Db 1149 GATGACAGCGCTTACGAGAGGTGCCAACAGGCTTCTGGGCTTCAATACGAGCGG 1208
 QY 405 ProSerValLeuAspSerIleGlyGluGlyPheSerPheGlnProLysLeuArgSerPro 424
 Db 1209 CCGTCTGCTCTGAGACGATCAAGAGAGGCTTCTCTTCCAGCCCAAGCTGCTCACCC 1268
 QY 425 ArgArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPheGlu 444
 Db 1269 AGCGCCCTTCAACAGTAGAGCCCGGGGTCCCGTCAAGCCCTCAAGTTCTCCCTTTGAG 1328
 QY 445 GlyPheArgProSerSerLeuProGluProGluProGluProLeuProLeuProLeu 464
 Db 1329 GGGTTTGGCCCGAGCCCGAGCTTCCGAGGCCAGAGCTACTTACTTCACTCTCTG 1388
 QY 465 ProProProProProSerThrThrAlaProLeuProIleArgProProSerGlyThrLys 484
 Db 1389 CCACCGCGCGCGCTTCCAGCACCGCGCCCTCTCCCATCCGCCCCCTCAAGGACCAAG 1448
 QY 485 LysSerLysArgGlyArgGlyArgProGlyArg 495
 Db 1449 AAGTCCAGAGGAGGAGCGGTGGGTCCAGAGGCGC 1481

RESULT 2

US-08-966-316-10
 : Sequence 10, Application US/08966316
 : Patent No. 5932445
 : GENERAL INFORMATION:
 : APPLICANT: Lal, Preeti
 : APPLICANT: Au-Young, Janice
 : APPLICANT: Reddy, Roopa
 : APPLICANT: Murthy, Lynn B.
 : APPLICANT: Mathur, Preeti
 : TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
 : STREET: 3174 Porter Drive
 : CITY: Palo Alto
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94304
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FastSeq for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/966,316
 : FILING DATE: Herewith
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER:
 : FILING DATE:
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Billings, Lucy J.
 : REGISTRATION NUMBER: 36,749
 : REFERENCE/DOCKET NUMBER: PF-0424 US
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650-855-0555
 : TELEFAX: 650-845-4166
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 10:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1637 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : IMMEDIATE SOURCE:
 : LIBRARY: SKINBIT01
 : CLONE: 1869688
 : US-08-966-316-10

Alignment Scores:

Pred. No.: 6,27e-159 Length: 1637
 Score: 1947.50 Matches: 407
 Percent Similarity: 90.89% Conservative: 2
 Best Local Similarity: 90.44% Mismatches: 34
 Query Match: 74.50% Indels: 13
 DB: 2 Gaps: 4

US-09-762-258-2 (1-495) x US-08-966-316-10 (1-1637)

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QY 9 G1YAlaG1YAlaAlaMeValAlaValAlaPheAspLeuAspLeuGluThrGluGluGluSer 28
Db 180 GGGGGCCGCGCCGCGCATGCGCGCGTGTATTGATTGATTGAGAGCGAGGAGGAGGAGC 239
QY 29 G1uG1yG1uG1yG1uPProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArg 48
Db 240 GAGGGCGAGGGCGAGCGAGCGAGCTCAGCCCGGAGCGCAGTCTCCCTTGCAGAGTTGAG 299
QY 49 AlaAlaG1yLeuGluPProValG1YH1sTyrG1uG1uValG1uLeuThrG1uThrSerVal 68
Db 300 GCACTGGCCCTAGAGCCCTGTGGACACTATGAGAAGGTGGAGCTGACTGAGACCGAGCTG 359
QY 69 AsnValG1yPProGluArgG1yG1yProH1sCysPheGluLeuLeuArgValLeuG1yLys 88
Db 360 AACCTTGCCCGAGCGCGCATCGCGCCCGCATGCTTGAGCTGCTGCTGCTGCGGAG 419
QY 89 G1YG1YTYG1YLYSValAlaPheGluValArgPysValG1uG1yThrAsnLeuG1yLys1le 108
Db 420 GGGGGCTATGGCAGAGGTGTTCCAGGTGGAGAGGTGGAGGAGGAGCAGCAGCAGATATA 479
QY 109 TyrAlaMetLysValLeuArgLysAlaLys1leValArgAsnAlaLysAspThrAlaH1s 128
Db 480 TATCCCATGAAGTCTTAAGAGAGCGCAAAATTTGTGGCATGTGCAAGACACAGCAC 539
QY 129 ThrArgAlaGluArgAlaGluLeuGluSerValLysH1sProPhe1leValG1uLeuAla 148
Db 540 ACAGGGCTAGCGCGAAGCATTTCTAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 599
QY 149 TyrAlaPheGluThrG1yG1yLysLeuTyrLeu1leLeuG1yCysLeuSerG1yG1yG1 168
Db 600 TATCCCTTCCAGATGTGTGGAGAACTTACTCTTCTTGTGATGCTGCTGCTGCTGCTG 659
QY 168 uLeuPheThrH1sLeuGluArgG1yG1y1lePheLeuGluAspThrAlaCysPheTyrLe 188
Db 660 GCTCTTCACGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 719
QY 188 uAlaG1u1leThrLeuAlaLeuG1yH1sLeuH1sSerGluG1yTyr1leTyrArgAspLe 208
Db 720 GAGTGAATGACGCTGGCGCTGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 779
QY 208 uLysPProGluAsn1leMetLeuSerSerG1uG1yH1s1leLysLeuThrAspPheG1yLe 228
Db 780 CAAAGCCGAGAGACATCAGCTCAGACAGCGGCGCAGATCAAACTGACCGACCTTGGACT 839
QY 228 uCysLysGluSer1leH1sG1uG1yAlaValAlaThrH1sThrPheCysG1yH1s1leG1y 248
Db 840 CTGCAAGAGAGTCAATCAATGAGGGCGCGTCACTCAACACCTTCTGCGGCGACCATGAG 899
QY 248 rMetAlaPProGlu1leLeuValArgSerG1yH1sAsnArgAlaValAspTyrTrpSerLe 268
Db 900 CATGGCCCTGAGATTCTGGTGGCGCAGTGGCGCAACCGGGCTGTGAGCTGTGGAGCCT 959
QY 268 uG1YAlaLeuMetLysAspMetLeuThrG1ySerProPheThrAlaGluAsnArgLys 288
Db 960 GGGGGCCCTGAGTGAATGACATGCTCACTGAGATCCCGCCCTTCAACCGAGAGAGACCG 1019
QY 288 sLysThrMetAspLys1le1leArgG1yLysLeuAlaLeuProProTyrLeuThrProAs 308
Db 1020 GAAAGACATGATGAATCATCAGGGGCGAGCTGCGCCCTTCACTCACTCACTCACTCA 1079
QY 308 pAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArg1leG1yG1yG1 328
  
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Db 1080 TGCCCGGAGACTTGTCAAAAAGTTTCTGAAACCGAATCCAGCCAGCGGATGGGGGTG 1139
QY 328 YProG1yAspAlaAlaAspValG1uArgH1sProPheArgH1sMetAsnTrpAspAs 348
Db 1140 CCCAGGGAGAGCTGCTGATGTGAGAGACATCCCTTTTCCGGCACATGAATTTGGAGCA 1199
QY 348 pLeuLeuAlaTrpArgValAspProPheProArgProCysLeuGluSerG1uGluAspV 368
Db 1200 CTTCTGGCTGGCGGTGTGAGNCCCTTTCAAGGCCCTGTCTGCACTCAGAGAGAGCT 1258
QY 368 aLysGluPheAspThrArgPheThrArgGluThrProValAspSerProAspAspThrA 388
Db 1259 --GAGAGTTTGTATACCCGCTTCAACCGGACAGCGCGGTGACAGTCTGATGACAG 1316
QY 388 lAsnSerGluSerAlaAsnGluAlaPheLeuG1yPheThrTyrValAlaProSerVal 408
Db 1317 C-CTCAGCGAGAGTGTCAACAGGCTTCTGCGGTT-ATAATAGTGGCGG-TCGTCC 1373
QY 408 euAspSer1leLysG1uG1yPheSerPheGluProLysLeuArgSerProArgArgLeuA 428
Db 1374 TGAGCAG-ATCAGAGAG--TTCTCTTACGCCAAGT-----GGGTCAACAGGCGCTC 1423
QY 428 snSerSerProArgValProValSerProLeuLysPheSerProPheGluG1yPheArgP 448
Db 1424 AANATAGCCCGGG--TCCGTAGGCC--TCAAGTTTCCCTTMAAGGTTCCGCCA 1477
QY 448 roSerProSerLeuPProGluPProThr 456
Db 1478 GCCACCTTMCNGGCCAGAGAGTACT 1503

RESULT 3
US-09-817-310-1
; Sequence 1, Application US/09817310
; Patent No. 6534311
; GENERAL INFORMATION:
; APPLICANT: Stewart, Mary
; APPLICANT: Kozma, Sarah
; APPLICANT: Thomas, George
; TITLE OF INVENTION: Drosophila melanogaster P70 S6 Kinase
; FILE REFERENCE: 4-20971/A
; CURRENT APPLICATION NUMBER: US/09/817,310
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 09/230,247
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2556
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-817-310-1

Alignment Scores:
Pred. No.: 4.3e-116 Length: 2556
Score: 1455.00 Matches: 309
Percent Similarity: 66.73% Conservative: 52
Best Local Similarity: 57.12% Mismatches: 115
Query Match: 55.66% Indels: 65
DB: 4 Gaps: 10

US-09-762-258-2 (1-495) x US-09-817-310-1 (1-2556)

QY 13 AlaMetAlaAlaVal-----PheAspLeu-----AspLeuGlu 23
Db 471 GCATGGCGAGCTGAGCGATCCAGCGAAGCTTTCAGCTGAGCTGACGACCTGGAA 530
QY 24 ThrGluGluG1ySerGluG1yGluG1yPro-----GluLeuSerProAlaAsp 40
Db 531 CTGCGAGAGAGAGAGCGGAGAGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 590
QY 41 AlaCysProLeuAlaGluLeuArgAlaAlaG1yLeuGluProValG1yH1sTyrGluGlu 60
Db 591 CTAGAACCG-----GAATTGTATTAATCTGACCAAGACAGACAGAGAGAGAGAGAG 644
  
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QY	61	ValGluLeuThrGluThrSerValAsnValGlyProGluIleArg1ProHisGlySerPhe	80
Db	645	ATACAGCTCTCGCAGAGAGATTTATCCAGGTAAATATCAAGCTGGACCCAGACATTT	704
QY	81	GluLeuLeuArgValIleuGlyLysGlyGlyTyrGlyLysValPheGlnValArgLysVal	100
Db	705	GAGCTCAAGAAAGTCTCTGGCAAAAGCGGTATATGGCAAAAGTATTTACAGTGGCAAGACC	764
QY	101	GlnGlyThrAsnLeuGlyLysIleTyrAlaMetLysValIleuArgLysAlaLysIleVal	120
Db	765	GCTGACACGAGATGCTTAACAAATATTTGGCATGAAGTCTCAAAAGCATCAATTCATGGT	824
QY	121	ArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLys	140
Db	825	ACCATCAAAAGACACAGCGCACCCGCGCGCCCAATATCTCGAGCGCATCTTCAG	884
QY	141	HisProPheIleValGluLeuAlaTyrAlaPheGlnTrnGlyLysLysLeuTyrLeuIle	160
Db	885	CATCCCTTCATAGTGGAGCTAGTTATTCCTTCACGACAGACGAAACCTATACCTTATA	944
QY	161	LeuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuGluuArgGluGlyIlePheLeu	180
Db	945	CTTGAAATATCTCAGCGGTGGAGAGCTGTTCATGCTTTGGAGCGGAGCGCATCTTCTTA	1004
QY	181	GluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisIleuHisSer	200
Db	1005	GAGATACACATGCTTCTATCTATAGCAAAATCATTTTGCCCTTGGCCATCTACACAA	1064
QY	201	GlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHis	220
Db	1065	CTGGGCATCATCTTACCGGAGTCTGAAGCCCGAAATATCTGCTGAGACACAGGACAT	1124
QY	221	IleLysLeuTrnAspPheGlyLeuCysLysGluSerIleHisGluGlyAlaAlaThrHis	240
Db	1125	GTGAAGCTCAAGCATTTTGCACTGGACGTGCAGAGACACATACAAAGCGATTTGTCAACCA	1184
QY	241	ThrPheCysGlyThrIleGlnTyrMetAlaProGluIleLeuValArgSerGlyHisAsn	260
Db	1185	ACCTTCTGGCGCACAAATTGAAGTACATGCACCTGAATTTGACACAGAGTGGCCATGCG	1244
QY	261	ArgAlaValAspTrpTrpSerLeuGlyValAlaLeuMetTyrAspMetLeuThrGlySerPro	280
Db	1245	AAAGCAGTCGACTGCTGTCTACTGGCCGCTCTCATGTTGACATCTCACAGAGTCCCA	1304
QY	281	ProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAla	300
Db	1305	CCCTTCAACCGCGAATGCGAAGAGACATCGAGACATTTCTGAAGCCAGAGCTCAAT	1364
QY	301	LeuProPheTyrLeuThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsn	320
Db	1365	CTGCCAGCCTACCTCACACCGGAACCGAGGATCTCGTGGCGCTGATGAAGCGGAG	1424
QY	321	ProSerGlnArgIleGlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhe	340
Db	1425	GAACCTCAGCCCTTGGCGAGCGGACCCGAGATGCGCGCGCTTCAATATCACCCATTC	1484
QY	341	PheArgHisMetLeuTrnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgPro	360
Db	1485	TTCAAAACACGTCAGCTGGAGCGATGTCTCCGCCAAGCCCTCGAGCCGCCATATAAACCG	1544
QY	361	CysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnTrnPro	380
Db	1545	CTCTTGAAACACGAGATGATGTCTCAGATTCATATAAAATTCACAAAGCAATTCCA	1604
QY	381	ValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGlnAlaPheLeuGlyPhe	400
Db	1605	GTGATTTCCCTGATGATACAAACGTAAAGCAAGTGCATTTAATTTTCAAGATTTC	1664
QY	401	ThrTyrValAlaProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLys	420
Db	1665	ACCTACGTTGACCTCGATCTGATCTGAGGATATGATCGG-----GCCAACCGAGTCCA	1718

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QY      421 LeuArgSerProAlaGly-LeuAsnSerProArgValProvalSer----- 436
        |||||
Db       1719 GCAGCGCTCCCAACAGCAGCTTCCAGCAGCAGCAGCAGCAGCTTCGACATGC 1778
        |||||
QY      437 -----ProLeuLysPheSerProFheGluGlyPhe----- 446
        |||||
Db       1779 CCATGCCGCAATGTGGGCGCCAAATGCCGCTGTGACCATGACAGCGTCATTGCGCAGCGATC 1838
        |||||
QY      447 -----ArgProSe 449
        |||||
Db       1839 CGGATGTTTGACAGAGCACGCCGCCGATCATCATGACAGACATTTGGCGCCGCTTCATC 1898
        |||||
QY      449 rProSerHeuProGluProThrGlu-----LeuPro-----LeuProPr 462
        |||||
Db       1899 GCCGGCGGACAGACGAGATGATGAAGTAGCAGAGGTCTGCGCATGTGCTTAAGGCTGAGAGCG 1958
        |||||
QY      462 OLeuLeuProProProProSerThrThraLaProLeuProIleargPro----- 479
        |||||
Db       1959 ATTGCTTCCCACAACCAACCAACCATCCATCCGCTCGTTCCGTGCGAACCCAGCAACTG 2018
        |||||
QY      480 -----ProSerGlyThrLysIleSerLysArgIylarGlyAr 492
        |||||
Db       2019 CATCATAGCTTCTCTCTCCCTCAACCCCAAAAAAAAAAAAAAAAAAAAAAAG 2078
        |||||
QY      492 g 492
        |||||
Db       2079 A 2079
        |||||

RESULT 4
US-08-749-902-4
; Sequence 4, Application US/08749902
; Patent No. 5985635
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN SERINE/THREONINE
; NUMBER OF INVENTION: PROTEIN KINASES
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/749,902
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0150 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: Consensus
; US-08-749-902-4

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Alignment Scores:

Pred. No.: 2-21e-110 Length: 1607
 Score: 1385.50 Matches: 285
 Percent Similarity: 70.65% Conservative: 40
 Best Local Similarity: 61.96% Mismatches: 69
 Query Match: 53.00% Gaps: 67
 DB: 2 Indels: 10

US-09-762-258-2 (1-495) x US-06-749-902-4 (1-1607)

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QY 86 LeuGlyysgIyglYrGlylsValpHeGlnValArglysValGlnGlyThrAspHeu 105
DB 227 CTGGGGGAGGGCGGCTCATGCCAGTGACAGCTGC-----ATTAACTG 271
QY 106 -----GlylsleIeYrAlaMetLysValLeuArg-----LysAla 117
DB 272 ATCCACGACGAGGAGTACCCGTCGCAAAATCATGTTTTTTTTCAGAGCCACATTCGGAGC 331
QY 118 LysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGlu 137
DB 332 AGGGTTTTCAGGAGGAGTGTCTGTACCAAGTGCAGGAGCACAGAAAGTCTTACAG 391
QY 138 SerVallybHsPhePheIleValGluLeuAlaTyrAlaPheGlnThrGlyLysLeu 157
DB 392 CTGATTAGTTC-----TTGAGAGAGAGAGACCGCTTC 424
QY 158 TyrIleuIleLeuGlyCysLeuSerGlyGlyLeuPheThrHisLeuGluArgGluGly 177
DB 425 TACTGTGTTTGAAGAAGATCGGGAGAGCTCCATCTCGAGCCACATCCACAGAGCCGG 484
QY 178 IlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHis 197
DB 485 CACTTCACACAGCTGAGAGCCAGCGTGTGTGAGAGAGCTGCGCACGCTTGACTT 544
QY 198 LeuHisSerGlnGlyIleIleTyrArgAspLeuysProGluSerIleMetLeuSerSer 217
DB 545 CTGATACACAAAGCATGCGCCACAGGAGACTTAAGCCGGAAGAAACATCTCTGTAGACAC 604
QY 218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228
DB 605 CCCACACAGGATCTCCCGGAGAGATCTGTGACTTGACCTGGGAGCGGATCAAACTC 664
QY 229 -----CysLysGlySerIleHisGlnGlyAla-ValThrHisThrPheCysGlyTh 245
DB 665 AACGGGAGACTGCTCCCTCAT-CTCCACCCCGAGAGCTGCTCACTCCG-----TGGGCTC 717
QY 245 rIleGlyTyrMetAlaProGluIle----- 253
DB 718 GGGGAGTATCATGCCCCCGAGAGTATGAGAGGCTTCAGAGAGGATTCATTCACGA 777
QY 254 -----LeuValArgSerGlyHisAs 260
DB 778 CAAGCGCTGACCTGTGAGAGCTGAGCGTCAATCTGTATATCTACTCTACGCGCTACCC 837
QY 260 nArgAlaValAsp---ThrTrpSer-----LeuGlyAlaLeuMetTyrAspMetIle 276
DB 838 GCCCTTGTTGGCGCGCTGTGTGGAGCGACATCGCGCTGTGGAGCCGCTATATGACAGATGCT 897
QY 276 uThrGlySerProPheThrAlaGluAsnArgLysIleThrMetAspLysIleIleArg 296
DB 898 CACTGATGCGCGCTTATCCCGACAGAAACCGGAAGAAACATGATAGATCATCAG 957
QY 296 gGlyLysLeuAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysLysbH 316
DB 958 GGGCAAGCTGGCACTGCCCTTACCTTACCCAGAGATGCGCGGAGACCTTGTCAAAAAGTT 1017
QY 316 eleuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaLysValG 336
DB 1018 TCTGAAGCGAATCCACGCGAGGATTGGGGTGGCCCGAGGAGTCTGTATATGCA 1077
QY 336 nArgHisProPhePheArgHisMetAsnTrpAspAspLeuLeuAlaTrpArgValAspPr 356

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DB 1078 GAGCATCCCTTTTTCGGGACATGATTTGGAGAGACACTTCTGGCCCTGCGCTGTGACCC 1137
QY 356 oProPheArgProCysLeuGlnSerGluAspValSerGlnPheAspThrArgPheTh 376
DB 1138 CCCCTTACGCGCCCTGTCTGTGAGTCAAGAGAGAGAGAGCTGAGCGAGTTTATACCCGCTTAC 1197
QY 376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGlnSerLysIleAsnGlnAl 396
DB 1198 AGGCGACACCGCGGTGAGAGTCTGTATGACAGCCCTCAGAGAGAGTGCACACAGGC 1257
QY 396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGlnGlyPhe 416
DB 1258 CTTCCTGGGCTTCAATACATCGGCGCGCTGTCTGTGAGACAGATCAAGAGAGGCTTCTC 1317
QY 416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVal 436
DB 1318 CTTCAGCCCAACCTGCTGACCCAGGCGCTCAACAGAGGCCCGGGTCTCCCGTACG 1377
QY 436 rProLeuLysPheSerProPheGlnGlyPheArgProSerProSerLeuProGluProTh 456
DB 1378 CCCCCTCAAGTTCTCCCTTTTGAAGGGTTTGCGCCACAGCCAGCTGCGGAGGCCAC 1437
QY 456 rGluLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuPr 476
DB 1438 GAGCTAACCTTCACTCTCACTCTGTCACCGCGCGCTCGACACCGCCCTCTCC 1497
QY 476 oIleArgProProSerGlyThrLysSerLysArgLysArgGlyArgProGlyArg 495
DB 1498 CATCTGTCCTCCCTTCAAGGACCAAGAGTCCAGAGGAGGCGTGGCGTCCAGGGCT 1555

RESULT 5
US-09-016-434-126
; Sequence 126, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016.434
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 126:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1607 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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IMMEDIATE SOURCE:
LIBRARY: COMFET02
CLONE: 1309709
US-09-016-434-126

Alignment Scores:

Score:	2,21e-110	Length:	1607
Percent Similarity:	1385.50	Matches:	285
Best Local Similarity:	70.65%	Conservative:	40
Query Match:	61.96%	Mismatches:	69
	53.00%	Indels:	67
		Gaps:	10

US-09-762-258-2 (1-495) X US-09-016-434-126 (1-1607)

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QY 86 LeuGlyysGlyTyrGlyLysValPheGlnValArgLysValGlnGlyThrAspLeu 105
DB 227 CTGGGGAGGGGCGCTCATGCGCGAGTGCAGACCTGC-----ATTAACTTG 271
QY 106 -----GlyLysIleTyrAlaMetLysValLeuArg-----LysAla 117
DB 272 ATCAACAGCCAGAGAGTACNCCGTCANATCATTTTTCACAGCCACATTCGAGC 331
QY 118 LysIleValArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGlu 137
DB 332 AGGGTTTTCAGAGGAGTGCAGATGCTGTACCAAGTGCAGAGGACACAGAGAACGTCCTAGAG 391
QY 138 SerValLysHisProPheIleValIleGluLeuAlaTyrAlaPheGlnThrArgLysLeu 157
DB 392 CTGATGAGTTC-----TTCCAGAGGAGAGACCGGCTTC 424
QY 158 TyrLeuIleLeuGluCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGly 177
DB 425 TACCTGGTGTGTTGAGAGATGCGGGAGAGGCTCCATCTCGAGCCCATCCAGAACGCGCG 484
QY 178 IlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHis 197
DB 485 CACTTCAACAGAGCTGAGGCGCAGCGTGTGTGAGAGACGTGGCCAGCGCTTGGACTTT 544
QY 198 LeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSer 217
DB 545 CTGCATTAACAAGAGCATCCGCCACAGGAGCATTAAGCCGAGAAACATCCCTGTGAGAC 604
QY 218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228
DB 605 CCCAACAGAGCTTCCCGCGAGAAATCTGACTTCACTTCCAGGAGGAGGAGCATCAAACTC 664
QY 229 -----CysLysGluSerIleHisGluGlyAla-ValThrHisThrPheCysGly 245
DB 665 AAGCGGAGCTGCTCCCTAT-CTCCACCCCGAGCTGCTCACTCCG-----TCCGCTC 717
QY 245 rIleGluTyrMetAlaProGluIle----- 253
DB 718 GAGCGAGTACATGCCCCCGAGAGTGTGAGGCTTCAGAGAGGAGGCTAGACTACGA 777
QY 254 -----LeuValArgSerGlyHisAs 260
DB 778 CAGCGCTGCGAGCTGTGAGAGCTGGCGCTCATCTGTATATATCTTACTACGCGCTACCC 837
QY 260 nArgAlaValAsp---TyrTrpSer-----LeuGlyAlaLeuMetTyrAspMetIle 276
DB 838 GCCCTTGCGGGCGCGTGTGGAGGAGCATGCGCGCTGGAGCCGCTGATGTAGCAKATGCT 897
QY 276 uThrGlySerProPheThrAlaGluAsnArgLysLysThrMechAspLysIleIleLeu 296
DB 898 CACTGAGATCCCGCCCTTACCCGAGAAACCGGAGAAACCAATGATTAAGATCACTCAG 957
QY 296 gGlyLysLeuAlaLeuProGlyTyrLeuThrProAspAlaArgAspLeuValLysLysPhe 316
DB 958 GGGGAACTGGCACTNCCCTTACCTCAACCCAGAGTCCCGGAGCTTGTCAAAAAGTT 1017
QY 316 eLeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValGlu 336

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DB 1018 TCTGAACGAGATCCAGCCAGCGGATTGGGGGTGGCCAGGGGAGTCTGTAGTGC 1077
QY 336 nArgHisProPhePheArgHisMetAsnTrpAspLeuAlaIleTrpArgValAspPr 356
DB 1078 GAGACATCCCTTTTCCGACATGAATTGGAGCGACTTTCGCTGCGCTGTGGAGCCC 1137
QY 356 oProPheArgProCysLeuGlnSerGluGluAspLysSerGlnPheAspThrArgPhe 376
DB 1138 CCGTTTCAGCCCTGCTCTCACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1197
QY 376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGln 396
DB 1198 ACGGACAGCGCGGTGAGCAGTCTGATGACACAGCCCTCAGCGAGAGGCCAACGAGC 1257
QY 396 aPheLeuGlyPheThrTyrValAlaProSerAlaLeuAspSerIleGlyGlnGlyPhe 416
DB 1258 CTTCCTGGCTTCACTACATGAGCGCGCTCTCTCTGACACATCAAGAGAGGCTTTC 1317
QY 416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerProArgValProValSe 436
DB 1318 CTTCAGAGCCAGAGTGCCTGACACAGAGGCTCAAGAGTACCCCGGCTCCGCTCAG 1377
QY 436 rProLeuLysPheSerProPheGlnGlyPheArgProSerProSerLeuProGluPro 456
DB 1378 CCCCCCTCAAGTTCTCCCTTTTGAAGGGGTTTGCGCCAGCCCAAGCTGCGAGGCCAC 1437
QY 456 rGluLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuPr 476
DB 1438 GAGGCTACTTCACTTCACTTCTGACCGCGCGGCTTGCACACCGCCCTTCTCC 1497
QY 476 oIleArgProProSerGlyTyrLysSerLysArgGlyArgGlyArgProGlyArg 495
DB 1498 CATCCGTCGCCCTCCAGGAGCAAGAGTCAAGAGGAGGCGTGGGCGCTCCAGAGGCGT 1555

```

RESULT 6

US-09-016-434-118

Sequence 118, Application US/09016434

Patent No. 6500938

GENERAL INFORMATION:

APPLICANT: Janice Au-Young

APPLICANT: Jeffrey J. Seilhamer

TITLE OR INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

TITLE OR INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSER: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016.434

FILING DATE: HEREWITH

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Zeiler, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0002 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 855-0555

TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 118:

SEQUENCE CHARACTERISTICS:

/	LENGTH:	669 base pairs
/	TYPE:	nucleic acid
/	STRANDEDNESS:	single
/	TPOLOGY:	linear
/	IMMEDIATE SOURCE:	
/	LITERARY:	BRAINOT11
/	CLONE:	1290913
US-09-016-434-118		
 Alignment Scores:		
Pred. No.:	1.29e-72	Length: 669
Score:	942.00	Matches: 204
Percent Similarity:	90.71%	Conservative: 1
Best local Similarity:	90.27%	Mismatches: 19
Query Match:	36.04%	Indels: 7
DB:	4	Gaps: 1
 US-09-762-258-2 (1-495) x US-09-016-434-118 (1-669)		
Qy	ArshrgAlaaRgsIyaLaGIyAlaalaMetAlaAvalPheAspLeuaspLeuglunthr	24
Dd	2 CGAGCGGCGCGCNGGGGC-GGCGCGCCAT-NGGGCGGTGTGAATTGGATTNNAGACG	59
Qy	25 GluGlunGIysertglunGIyglunGIyupProglunSerProalAspAlaCyseProleu	44
Dd	60 GAGAAAGCGACGAGGGCGAGGGCGAGCCAGAGCTCAACCGCCAGCATGTCCTT	115
Qy	45 AlaGlunEuARgAlaAlaGIyleugluProValIGlyHISTYrGLnGIwAlGIunEuThr	64
Dd	120 GCCGATTTAGGGCACCTGGCTCCAGACTTGAGCACTTAGAA-----GAGGG-ACT	177
Qy	65 GlunTherSeValanValGIyProglunArgIIegIyProHisCysePhelIuleuEuArg	84
Dd	173 GAGGCCAGCTGAAACGTGGCCAGAGCCGACATCGGGCCCCACTGCTTGAGCTGCTGGGT	232
Qy	85 ValIeuGIyVleglunGIyTrGIyVasIIPheGINValargLyValIGnGIyThrAsn	104
Dd	233 GTGTGTGGCGAAGGGGGCTTAGGCAAGGTGTTCAGAGNCGAANNGTGCAAGGACCAAC	292
Qy	105 IeuGIyLysIIeITraImetIySValIeuArgLyBaIalYslIevaIarGaSnalals	124
Dd	293 TTGGGCAAAATATATATCCATGAAGAICTTAAGAAAGGCCAAAATTTGTGGCAATTCACAG	352
Qy	125 AspThrAlahIsthIRgaIagIuaIgaEnIIeIeuGIuseRValIyHisEProPheIIe	144
Dd	353 GAACAAGCAACAACAAGGGCTGAGCGGAACATTCAGAGTCAAGTAACACACCCCTTAAT	412
Qy	145 ValGIuEuAlaITraIaphelInThrGIyVLSleyIyLeuIIeIeuGIuCYseIeu	164
Dd	413 GTGAAGNCGCCATACCTCTTCAGAGCTGTGGCAAACCTAACCCCATCTTGAGTNCCTC	472
Qy	165 SerGIyGIyGIuIueuTherHIsIeuGIuARGIunGIyIIepHeIeuIuAspThrala	184
Dd	473 AGTGTGTGGCAGCTCTTCACGATCTGAGCAGAGGGGACATCTCTTGAAAGATAAGGCC	532
Qy	185 CysEphTyriEuAlaGIuIIepThreulAlaIeuGIyHISleuHISserGINglyIle	204
Dd	533 TGTTTC-TACNAGCTAGATCAAGCTGGGCTGGGCCATCT-CATCTCCAAGGATCATC	590
Qy	205 TyrARgAspIeuIySProglunsnIIexIleuSerSerGINglyHISIIeIyaleuThr	224
Dd	591 TACCGGGAACCTCAAGCCGAGAAACATCATGTCAAGCAGCGGGCCACATCAACTGANC	655
Qy	225 AspPhelGIyIeuCYsIyS 230	
Dd	651 GAAITTTGAACTCTGCAAG 668	
 RESULT 7 US-09-031-295-1 Sequence 1, Application US/0901295 Patient No. 6326181 GENERAL INFORMATION: APPLICANT: LANG, Florian		

```

APPLICANT: WALDEGGER, Tubingen
TITLE OF INVENTION: CELL VOLUME-REGULATED HUMAN KINASE H-SGK
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/031,295
FILING DATE: 26-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 197-08-173.8
FILING DATE: 28-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 058315/0123
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5339
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2370 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 43..1335
US-09-031-295-I

Alignment Scores:
Pred. No.: 4,16e-60 Length: 2370
Score: 806.50 Matches: 172
Percent Similarity: 61.348 Conservative: 66
Best Local Similarity: 44.338 Mismatches: 111
Query Match: 30.858 Indels: 39
DB: 4 Gaps: 12

US-09-762-258-2 (1-495) x US-09-031-295-1 (1-2370)

QY 33 GlnProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
Db 235 GAACCTGAAGACTATGATGATCCCAACCCCTTCTCT----- 267

QY 53 GluProValGlyHisIleTyrgluGluValAluLueuhrgIutHrserValAsnValGlyPro 72
Db 268 ---CCACCAGTCCTCTTCAGCAA-----ATCAACCTTGCGCG 300

QY 73 GluArgIleGlyProHisCys-----PhegluLeuLeuArgValIleugilylys 88
Db 304 TGCTGC---AATCCATCATGCTAAACATCTGACCTTCACTTCTGAAAGATGATGGAAAG 366

QY 89 GlyGlyItyrGlyIyValPhegluValArg---IysValGlnGlyThrAsnLeuGilylys 107
Db 361 GGAGGTTTGGAAAAGTTCTTTCAGCAAGACAACAAGGCAAGAAGTG----- 408

QY 108 IleTyralMetIyValIleuArgIyValIalysIleValArgAsnAlaIyAspThraIa 127
Db 409 TTTCTARGAGCTGAAGTTTACAGAGAAAGAACCAATCTCGAAAAAG---AAAGAGAGAGAG 465

QY 128 HisThrArgAlaGluArgAsnIle---LeuGluSerValIyHisProPheIleValGlu 146

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Db      466 CATATTAATGCGAGCGGAAATGTTCTGTGAAGATGTGAACACCTTCTCGTGGCC 525
Qy      147 LeuAlaIYAlaIpeGInThrGlyGlyLeuLeuLeuLeuLeuLeuLeuLeuLeu 166
      526 CTTCACTCTCTCTCTCCAGACTGCTGACAAATGTAATGTAATGTAATGTAATGTAATG 585
Qy      167 GlyGluLeuPheThrHisLeuGluLeuGluGlyLeuPheLeuGluLeuPheLeu 186
      586 GGAAGTGTTCATCAATCTCCAGAGGGAACGCTGCTTCTGGAACCAAGCGGCTGCTTC 645
Qy      187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleLeuTyr 206
      646 TATCTCTGTAATATGCAATGCAATGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 705
Qy      207 AspleuLeuProGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 226
      706 GACTTAAACCAAGAAATATTTGCTGATTCACAGGAGACATTCCTGCTTACGATTC 765
Qy      227 GlyLeuGlyLeuGluSerIleHisGluGlyAlaValaThrHisThrPheCysGlyThr 246
      766 GGAATCTGCAAGGAGCAATTCGAACACACACACACACACACACACACACACACAC 825
Qy      247 GlyTyrMetAlaProGluLeuLeuValaLysSerGlyHisAsnArgAlaValaAsp 266
      826 GAGTATCTCCACCTGAGGCTTCATTAATGACAGCTTATGACAGAGCTGAGCTGCTG 885
Qy      267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGluLeu 286
      886 TGCCTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 945
Qy      287 ArgLysIleThrMetAspLysIleLeuArgGlyLeuLeuAlaLeuProPheTyrLeu 306
      946 AAGCTGCAATATGACGACCAATTCGTAACACACCTTCGAGCTGGAACCAATATTA 1005
Qy      307 ProAspAlaArgAspLeuValIleLysLysPheLeuLysArgAsnProSerGlnAla 326
      1006 AATTCCGCAAGACACCTCCGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
Qy      327 GlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsn 346
      1063 GGGGCGCAAGATATCTTCATGAGATTAAGATCAATCTTCTTCTTCTTCTTCTTCT 1122
Qy      347 AspAspLeuLeuAlaIleTyrAlaValaAspProPheArgProCysLeuGlnSer 366
      1123 GATGATCTCATTAATAAGAGATTATCTCCCTTTTAAACCAATGTAAGTGGCCCA 1182
Qy      367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381
      1183 GAGCTACGCACTTGAACCCGAGTTTACCGAAGAG---CTGTCTCCCAATCTCCATTGG 1239
Qy      382 AspSerProAspAsp-----ThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeu 398
      1240 AAGTCCCTGACAGCGCTCCGTCACAGCGGCTCAAGAGAGCTCGGAGGCTTCTTA 1299
Db      399 GlyPheThrTyrValaAlaProSer 406
      1300 GGCTTTTCTATGCGCTCCACG 1323

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RESULT 8

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US-08-712-709-6
Sequence 6: Application US/08712709
Patent No. 5863780
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

```

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; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,709
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-4166
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2311 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE: Consensus
; US-08-712-709-6

Alignment Scores:
Score: 8,886-60 Length: 2311
Percent Similarity: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39
DB: Gaps: 12

US-09-762-258-2 (1-495) x US-08-712-709-6 (1-2311)
Qy      33 GIUPROGILUESEPRQIALASPALACYSPPROLEUALAGLULEUARGALALAGLU 52
      202 GAGCTTGAAGCTTATGATGATGCAACCTTCTCTCT----- 234
Qy      53 GIUPROVALGILYHETRYGLUVALGULUEUTHRGUTHSERVALASVALGILYPRO 72
      235 ---CCACCAAGCTCTTCAAGCA-----ATCACTTGGCCCG 270
Qy      73 GLUARGILLEGYPHETIHCYS-----PHEGLULEUARGVALLEUGLYLYS 88
      271 TCGTCC---ATCTCATGCTPAACCATCTGACTTCACTTCTTAAGATGATCGAAG 327
Qy      89 GLYGLYTRYGLYLYSVALPHEGLINVALARG---LYSVALGILNYTHRASNLEUGLYL 107
      328 GGCAGTTTGGAAAGTTCTTCTACCAAGACACCAAGGCAAGAGTG----- 375
Qy      108 ILEIYRALMETLYVALLEUARGLYSALALYSILEVALAGSNALALYASPTHRAL 127
      376 TTCTATGAGTCAAGATTTCAGAGAAAGCAATCGAAGAAAG---AAGAGAGAGAG 432
Qy      128 HISTHARGALAGLARGASNILE---LEUGLUSERVALIYSHISPROPHETILEVAL 146
      433 CATATTAATGCGAGCGGAAATGTTCTGTGAAGATGTGAACACCTTCTCGTGGCC 492
Qy      147 LeuAlaIYAlaIpeGInThrGlyGlyLeuLeuLeuLeuLeuLeuLeuLeuLeu 166
      493 CTTCACTCTCTCTTCCAGACTGCTGACAAATGTAATGTAATGTAATGTAATGTAATG 552
Qy      167 GlyGluLeuPheThrHisLeuGluLeuGluGlyLeuPheLeuGluLeuPheLeu 186
      553 GGAAGTGTTCATCAATCTCCAGAGGGAACGCTGCTTCTGGAACCAAGCGGCTGCTTC 612
Qy      187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleLeuTyr 206

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Db 613 TATGCTGTAATAGACAGAGCTTGGGCTACCTGATTCATGACATGACATGATGTTATAGA 672
Qy AspleuylsProgluabnillemeleuserseinginyshileysleuthrAspHe 226
Db 673 GACTTAAACAGAGAAATATTTTGTATATTCACAGGAGACATGTCCTTACGACTTC 732
Qy 227 GlyleuCyalsgluserlilehisluglialavalThrHsThrPheCysGlyThrile 246
Db 733 GGACTCTGCAAGAGACATGAC 792
Qy 247 GluThrMetAlaProgluileleuvalargserglyhisasargalavalasPTrip 266
Db 793 GAGTATCTCGACAGAGCTCTTCATAGACGCTTATGACAGAGCTGAGCTGAGCTGG 852
Qy 267 SerleuGlialaleuMetTyrAspMetleuthrghlyserProProPheThrAlaGluasn 286
Db 853 TGCTGGAGCTGCTTGTATGAGAGTGTATGAGCTGCTGCTGCTGCTTATAGCGGAAC 912
Qy 287 ArglylyThrMetAspLysilelelearglylyleuvalaleuProProTyrleuthr 306
Db 913 ACAGCTGAATGTACGACACATTCCTGAAACAGCTCTCCAGCTGAAACCAATATTAACA 972
Qy 307 ProAspAlaArgAspLeuVallylsylPheleuylsargasnProserGlnargilegly 326
Db 973 AATCCGAGACACACCTCTCGAGGCTCTCTGAGAGAGACAGACAAACGCGCTC--- 1029
Qy 327 GlyGlyProgluAspAlaAlaAspValGlnargHisProPheArgHisMetAsnTrp 346
Db 1030 GGGGCGAAGATGATCTTCATGAGATGATGATGATGATGATGATGATGATGATGATG 1089
Qy 347 AspAspLeuAlaAlaTrpArgValAspProPheArgProCysleuGlnserGluGln 366
Db 1090 GATATCTCATATATTAAGAGATTAATCCCTTTTAACCAATGAGTGGGCCCAAC 1149
Qy 367 AspValserGlnPheAspThrArgPheThrArgGlnThrProVal----- 381
Db 1150 GACCTACGCGACCTTTGACCCGAGTTTACCGAAGG---CCTGTCGCCCACTCATTTGGC 1206
Qy 382 AsperProAspAsp-----ThrAlaleuSerGlnserAlaasnGlnAlaPheleu 398
Db 1207 AAGTCCCTGACAGGCTCTGTCAGCGCCAGCGTCAAGAGAGTGGCGAGGCTTTCTTA 1266
Qy 399 GlyPheThrTyrValAlaProSer 406
Db 1267 GGCCTTTCTATGCGCTCCACG 1290

RESULT 9
US-09-111-444-6
Sequence 6, Application US/09111444
Patent No. 6045792
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/111,444
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2311 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-111-444-6

Alignment Scores:
Pred. No.: 8,88e-60 Length: 2311
Score: 802.50 Matches: 172
Percent Similarity: 61.08% Conservative: 65
Best Local Similarity: 44.33% Mismatches: 112
Query Match: 30.70% Indels: 39
DB: 3 Gaps: 12

US-09-762-258-2 (1-495) x US-09-111-444-6 (1-2311)

Qy 33 GluProgluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaAlaGlyLeu 52
Db 202 GACCTGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 234
Qy 53 GluProValAlaIshTyrGluGluValGluLeuThrGluThrSerValaIshValGlyPro 72
Db 235 ---CCACCAAGCTCTTCTGACAA-----ATCAACCTTGGCGCG 270
Qy 73 GluArgileGlyProHisCys-----PheGluLeuLeuArgValaIshGlyLys 88
Db 271 TGCTCC---AATCTGATGCTAAACATGCTGACTTTCACCTCTTGAAGATGGGAAG 327
Qy 89 GlyGlyTyrGlyLysValaPheGlnValArg---LysValaGlnGlyThrAsnLeuGlyLys 107
Db 328 GGCAGTTTGGAAAGGTTCTTTCAGACACACACACACACACACACACACACACACACAC 375
Qy 108 IleTyrAlaMetLysValaLeuArgLysAlaLysIleValaArgAsnAlaLysAspThrAla 127
Db 376 TTCTATGAGCTCAAGGTTTACAGAGAAAGCAATCTGAAAAG---AAAGAGGAGAG 432
Qy 128 HisThrArgAlaGluArgAsnIle---LeuGlnSerValaIshHisProPheIleValaGlu 146
Db 433 CATATATATGCGAGAGGAGATGTTCTGTGAAGAAGTGAAGACACCTTCTGCTGGCGC 492
Qy 147 LeuAlaTyrAlaPheGlnThrGlyGlyLysLysLysLysLysLysLysLysLysLys 166
Db 493 CTTCCTCTCTTCCAGAGCTGTCACAAATGTACTTGTCTTCACTCACTCACTTAAGGT 552
Qy 167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186
Db 553 GAGAGTTTGTTCACATCTCCAGAGGGAACCTGCTTCTGGAACCAAGGCTCGTTCC 612
Qy 187 TyrLeuAlaGluThrThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArg 206
Db 613 TATGCTGTAATAGACAGAGCTTGGGCTACCTGACATTCAGTGAACATCGTTATAGA 672
Qy 207 AspleuylsProgluabnillemeleuserseinginyshileysleuthrAspHe 226
Db 673 GACTTAAACAGAGAAATATTTTGTATATTCACAGGAGACATGTCCTTACGACTTC 732
Qy 227 GlyleuCyalsgluserlilehisluglialavalThrHsThrPheCysGlyThrile 246
Db 733 GGACTCTGCAAGAGACATGAC 792

QY 247 GlnTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTrp 266
 DB 793 GAGTATCTCGACCTGAGGCTCTCATTAAGAGCTGATGAGCTGCTGG 852
 QY 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
 DB 853 TGCCCTGGAGAGCTGCTGTATGAGATGCTGTATGCGCTGCGCTTTTATACCGAACC 912
 QY 287 ArgLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeuThr 306
 DB 913 ACACCTGAAATGTAAGCAACATCTGACACAGCCCTCCAGCTGAAACCAATATTACA 972
 QY 307 ProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIleGly 326
 DB 973 AATCCCGAAGACACCTCTCGAGAGGCTCTCTGAGAGAGACAGACAAAGCCGCTC--- 1029
 QY 327 GlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsnTrp 346
 DB 1030 GGGGCAAGATGACCTCATGAGATTAAAGATCATGTCTTCTTCTTAATTAACTGG 1089
 QY 347 AspAspLeuLeuAlaTpaArgValAspProProPheArgProCysLeuGlnSerGluGlu 366
 DB 1090 GATGATCTCATTAATTAAGAGATTACTCCCTTTTAAACCAATGAGTGGGCGCCAAC 1149
 QY 367 AspValSerGlnPheAspThrArgPheThrArgGlnThrProVal----- 381
 DB 1150 GACCTAGCGGACCTTGAACCCGAGTTTACGAAAGAG---CTGTCCCAACTCCATTGGC 1206
 QY 382 AspSerProAspAsp-----ThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeu 398
 DB 1207 AAGTCCCTGACAGCGCTCTGTCACAGCGAGGTCAGAGAGATGCGAGGCTTCTTCTTA 1266
 QY 399 GlyPheThrTyrValAlaProSer 406
 DB 1267 GGCCTTTCCTATGCGCTCCCAAG 1290
 RESULT 10
 US-09-541-228-6
 ; Sequence 6, Application US/09541228
 ; Patent No. 6232077
 ; GENERAL INFORMATION:
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Hawkins, Phillip R.
 ; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: U.S.
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/541,228
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/712,709
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0118 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 2311 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

IMMEDIATE SOURCE:

LIBRARY:

CLONE: Consensus

US-09-541-228-6

Alignment Scores:

Pred. No.:	8,89e-60	Length:	2311
Score:	802.50	Matches:	172
Percent Similarity:	61.08%	Conservative:	65
Best Local Similarity:	44.33%	Mismatches:	112
Query Match:	30.70%	Indels:	39
DB:	3	Gaps:	12

US-09-762-258-2 (1-495) x US-09-541-228-6 (1-2311)

QY 33 GlnProGluLeuSerProAlaAspAlaCysProLeuAlaGluLeuArgAlaIleGlyLeu 52
 DB 202 GAGCCTGAGCTTATGAAATGCAACCTTCTCT----- 234
 QY 53 GlnProValGlyHisTyrGluGluValGluLeuThrGluThrSerValAsnValGlyPro 72
 DB 235 ---CAACCAAGCTCTTCAGCA-----ATCAACTTGGCCCG 270
 QY 73 GluArgIleGlyProHisCys-----PheGluLeuLeuArgValLeuGlyLys 88
 DB 271 TCGTCC---AATCCCATGCTTAACCATCTGACTTCACTTCTTAAAGTATGCGAAG 327
 QY 89 GlyGlyTyrGlyLysValPheGluValArg---LysValGlnGlyThrAsnLeuGlyLys 107
 DB 328 GCACTTTGGAAGAGCTTCTTACCAAGACCAAGGAGAAAGAGT----- 375
 QY 108 IleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAspThrAla 127
 DB 376 TTCATGACGATCAAGATTCTTACAGAAAGCAAGCAATCGAAGAAAG---AAAGAGGAGAG 432
 QY 128 HisThrArgAlaGluArgAsnIle---LeuGlnSerValLysHisProPheIleValGlu 146
 DB 433 CATATTATGTCGAGCGGAATGCTGTGTAAGAAATGAAAGACCCCTTCTGCTGGTGGC 492
 QY 147 LeuAlaTyrAlaPheGlnThrGlyLysLeuTyrLeuIleLeuGluCysLeuSerGly 166
 DB 493 CTTCACCTCTCTTCCAGCTGCTGACAAATTGACTTTCCTGACTACATTATAGGT 552
 QY 167 GlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPhe 186
 DB 553 GAGAGTGTGCTTACCATCTCCAGAGGAGAGCGTCTCTGAAACCAAGGCGCTGTTC 612
 QY 187 TyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyrArg 206
 DB 613 TATGCTGCTGAATGACCAAGCTGCTTGGGCTACCTGACTTCACTGAAACATGTTATAGA 672
 QY 207 AspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeuThrAspPhe 226
 DB 673 GACTTAAACAGAGAAATATTTGCTACATTACAGGAGCACTTGTCTTACAGACTTC 732
 QY 227 GlyLeuCysLysGlnSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIle 246
 DB 733 GACCTCTGACAGAGAAACATTGACACACAGCACACATCTCCCTTCTGTGGCAGCGG 792
 QY 247 GlnTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyrTrp 266
 DB 793 GAGTATCTCGACCTGAGGCTCTCATTAAGAGCTGATGAGCTGCTGG 852
 QY 267 SerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGluAsn 286
 DB 853 TGCCCTGGAGAGCTGCTGTATGAGATGCTGTATGCGCTGCGCTTTTATACCGAACC 912

DB 131 KOTAHRAERNTLESKHPIVELAFAFOTGKLYILECLSGSELTLEBEGFLEBT 190
QY 184 ACFTYLAETTLALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFC 243
DB 191 ACFTYLAETTLALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFC 250
QY 244 GTEYAPAEIYVSGHRAVDWMSLGALMYDMITGSPPTAERKKTMDKIRGKALAP 303
DB 251 GTEYAPAEIYVSGHRAVDWMSLGALMYDMITGSPPTAERKKTMDKIRGKALAP 310
QY 304 YLTPDARDLVKKEFLKXENPSQRTGGPGDAADVGRHPPFRHNMWDLAMRVDPPEPCLQ 363
DB 311 YLTPDARDLVKKEFLKXENPSQRTGGPGDAADVGRHPPFRHNMWDLAMRVDPPEPCLQ 370
QY 364 SEEDVQFOTRFRORPVDSPPDTALSESANQAFIGFTYVAVSVDISKEGFSPOPKLS 423
DB 371 SEEDVQFOTRFRORPVDSPPDTALSESANQAFIGFTYVAVSVDISKEGFSPOPKLS 430
QY 424 PRALNSPPVPSPLKFSPEGFRPSPLPEPTLPLPPLPPEPSTTAPPIRPPSGT 483
DB 431 PRALNSPPVPSPLKFSPEGFRPSPLPEPTLPLPPLPPEPSTTAPPIRPPSGT 490
QY 484 KSKRGGRGRGR 495
DB 491 KSKRGGRGRGR 502

RESULT 2

US-10-217-155A-16
Sequence 16, Application US/10217155A
Publication No. US20030065855A1
GENERAL INFORMATION:
APPLICANT: Barford, David
APPLICANT: Yang, Jing
APPLICANT: Hemmings, Brian A
APPLICANT: Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures and Methods for
FILE REFERENCE: 44236
CURRENT FILING DATE: 2002-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 333
TYPE: PRT
ORGANISM: Unknown Organism
FEATURES:
OTHER INFORMATION: Description of Unknown Organism: Sequence source
US-10-217-155A-16

Query Match 67.2%; Score 1756; DB 12; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-118; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RIGPHCFELLRLVYLGKGGYKVFQVRKVOGTNLGKIYAMKVLKRAKIVANAKDTAHTRAER 133
DB 1 RIGPHCFELLRLVYLGKGGYKVFQVRKVOGTNLGKIYAMKVLKRAKIVANAKDTAHTRAER 60
QY 134 NILSVKHPFIYELAVAFOTGKLYILECLSGSELTLEBEGFLEBTACFYLAETTL 193
DB 61 NILSVKHPFIYELAVAFOTGKLYILECLSGSELTLEBEGFLEBTACFYLAETTL 120
QY 194 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFCGTIYMAEI 253
DB 121 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFCGTIYMAEI 180

QY 254 LVRSCHRAVDWMSLGALMYDMITGSPPTAERKKTMDKIRGKALAPPLYTPDARDLV 313
DB 181 LVRSCHRAVDWMSLGALMYDMITGSPPTAERKKTMDKIRGKALAPPLYTPDARDLV 240
QY 314 KKFLENPSQRTGGPGDAADVGRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSQFDT 373
DB 241 KKFLENPSQRTGGPGDAADVGRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSQFDT 300
QY 374 RFTROTVDSPDDTALSESANQAFIGFTYVA 404
DB 301 RFTROTVDSPDDTALSESANQAFIGFTYVA 331

RESULT 3

US-10-217-574-16
Sequence 16, Application US/10217574
Publication No. US20040005687A1
GENERAL INFORMATION:
APPLICANT: Barford, David
APPLICANT: Yang, Jing
APPLICANT: Hemmings, Brian A
APPLICANT: Cron, Peter D
TITLE OF INVENTION: Kinase Crystal Structures
FILE REFERENCE: 44237
CURRENT FILING DATE: 2002-12-23
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2001-08-14
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-05-01
PRIOR FILING DATE: 2002-07-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 333
TYPE: PRT
ORGANISM: Unknown Organism
FEATURES:
OTHER INFORMATION: Description of Unknown Organism: Sequence source
US-10-217-574-16

Query Match 67.2%; Score 1756; DB 15; Length 333;
Best Local Similarity 100.0%; Pred. No. 2,4e-118; Indels 0; Gaps 0;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 RIGPHCFELLRLVYLGKGGYKVFQVRKVOGTNLGKIYAMKVLKRAKIVANAKDTAHTRAER 133
DB 1 RIGPHCFELLRLVYLGKGGYKVFQVRKVOGTNLGKIYAMKVLKRAKIVANAKDTAHTRAER 60
QY 134 NILSVKHPFIYELAVAFOTGKLYILECLSGSELTLEBEGFLEBTACFYLAETTL 193
DB 61 NILSVKHPFIYELAVAFOTGKLYILECLSGSELTLEBEGFLEBTACFYLAETTL 120
QY 194 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFCGTIYMAEI 253
DB 121 ALGHLHSOGIIYRDLKPENIMLSOGHIKLTDFGLCKESIHEGAVTHFCGTIYMAEI 180
QY 254 LVRSCHRAVDWMSLGALMYDMITGSPPTAERKKTMDKIRGKALAPPLYTPDARDLV 313
DB 181 LVRSCHRAVDWMSLGALMYDMITGSPPTAERKKTMDKIRGKALAPPLYTPDARDLV 240
QY 314 KKFLENPSQRTGGPGDAADVGRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSQFDT 373
DB 241 KKFLENPSQRTGGPGDAADVGRHPPFRHNMWDLAMRVDPPEPCLQSEEDVSQFDT 300
QY 374 RFTROTVDSPDDTALSESANQAFIGFTYVA 404
DB 301 RFTROTVDSPDDTALSESANQAFIGFTYVA 331

RESULT 4

Query Match 66.6%; Score 1740; DB 14; Length 525;
 Best Local Similarity 68.0%; Pred. No. 5,8e-117;
 Matches 349; Conservative 51; Mismatches 83; Indels 30; Gaps 8;

QY 1 MAAGRACAGCA-----MAAFDIDLETEGSGEGEPESPADACPLAE-LRA 49
 DB 1 MRRRRRRDGFYPPDFRHRBAEDMAGVFIDIDLOQPDAGSEDELE---EGQOLNEMDH 56
 QY 50 AGLEP-----VGHYEVELTETSYNVGPERIGPHCFELLYLKGKGYKGYKRYKQVNTL 105
 DB 57 GCGPPELGMHEHEKEKEISTSYNRPBEXKREPCFELLYLKGKGYKGYKRYKQVNTL 116
 QY 106 GKTYANKVLRKAKIVNACQFAHTRABRNILSVKPIVEAYAFQGTQKYLILECLIS 165
 DB 117 GKIFAKVKLKKAMIVNACQFAHTRABRNILSVKPIVEAYAFQGTQKYLILECLIS 176
 QY 166 GGELFPHLEREGFLEDTACFYLAETTLALGHASHGIIYRDLKPEINIMLSGGHKLTD 225
 DB 177 GGELFPHLEREGFLEDTACFYLAETTLALGHASHGIIYRDLKPEINIMLSGGHKLTD 236
 QY 226 FGJCKESIHEGAVTHFCGIIIEYMAPEILVRSGNRAVDWMSIGALMYDMLTGSPPTAB 285
 DB 237 FGJCKESIHDGVTHTFCGIIIEYMAPEILVRSGNRAVDWMSIGALMYDMLTGAPPTGE 296
 QY 286 NRKTMMDKIRGLALPVLTPDARLVKKFLKRNPSQRIIGGPGDAADVQRRPFRHN 345
 DB 297 NRKTTIDKILCKLNPFLYTOBARDLKRLKRNASTLGGPGDAGVQAHPPFRHN 356
 QY 346 WDDLAMRYDPPRPPCLQSEEDVSOQDTRFTRQTPVDSDDPDLSSANQALGFTYVAP 405
 DB 357 WDDLAMRYDPPRPPCLQSEEDVSOQDTRFTRQTPVDSDDPDLSSANQALGFTYVAP 416
 QY 406 STVDSIKXEGSPQPKLRSPRLNSPRVVSPLKTSFPR-----GFRPSPLE-PTLPL 460
 DB 417 STVDSIKXEGSPQPKLRSPRLNSPRVVSPLKTSFPR-----GFRPSPLE-PTLPL 476
 QY 461 PLLPPTPSTT-----APLPIRPP-SGTGSKK 487
 DB 477 ETSGIEQMDVTTSGEASALPIRQPSGPKYKQ 509

RESULT 7
 US-09-817-310-2
 ; Sequence 2, Application US/09817310
 ; Patent No. US20010042254A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stewart, Mary
 ; APPLICANT: Kozma, Sarah
 ; APPLICANT: Thomas, George
 ; TITLE OF INVENTION: Drosophila Melanogaster P70 Se Kinase
 ; FILE REFERENCE: 4-20971/A
 ; CURRENT APPLICATION NUMBER: US/09/817,310
 ; CURRENT FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 09/230,247
 ; PRIOR FILING DATE: 1999-04-16
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 637
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-817-310-2

Query Match 54.6%; Score 1428; DB 9; Length 637;
 Best Local Similarity 67.2%; Pred. No. 2.1e-94;
 Matches 279; Conservative 47; Mismatches 81; Indels 8; Gaps 4;
 QY 19 DDLLETESSBEGEP-ELSPADACPLAEALRAAGLEPCHYEVELTETSYNVGPERIGP 77
 DB 17 DDLLETESSBEGEP-ELSPADACPLAEALRAAGLEPCHYEVELTETSYNVGPERIGP 74
 QY 78 HCFELLRYLKGKGYKGYKRYKQVNTLKGKGYKGYKRYKQVNTLKGKGYKGYKRYKQVNTL 137
 DB 78 HCFELLRYLKGKGYKGYKRYKQVNTLKGKGYKGYKRYKQVNTLKGKGYKGYKRYKQVNTL 137

DB 75 KDFELKXVLKGKGYKGYKRYKQVNTLKGKGYKGYKRYKQVNTLKGKGYKGYKRYKQVNTL 134
 QY 138 SYKHEPIYELAVPOTGKULILECLSSGSEIFTLREBEGFLEDTACFYLAETTLALGH 197
 DB 135 AKHEPIYELAVPOTGKULILECLSSGSEIFTLREBEGFLEDTACFYLAETTLALGH 194
 QY 198 LHSOGIIVRDLKPEINIMLSGGHKLTDGJCKESIHEGAVTHFCGIIIEYMAPEILVRS 257
 DB 195 LHSOGIIVRDLKPEINIMLSGGHKLTDGJCKESIHEGAVTHFCGIIIEYMAPEILVRS 254
 QY 258 GGNRAVDWMSIGALMYDMLTGSPPTABNRKTMMDKIRGLALPVLTPDARLVKKFL 317
 DB 255 GGNRAVDWMSIGALMYDMLTGSPPTABNRKTMMDKIRGLALPVLTPDARLVKKFL 314
 QY 318 KNPESQIRIGGPGDAADVQRRPFRHNMDLAWRVDPFRPPCLQSEEDVSOQDTRFTR 377
 DB 315 KNPESQIRIGGPGDAADVQRRPFRHNMDLAWRVDPFRPPCLQSEEDVSOQDTRFTR 374
 QY 378 QTPVDSDDPDLSSANQALGFTYVAPSTVDSIKXEGSPQPKLRSPRLNSPR 432
 DB 375 QTPVDSDDPDLSSANQALGFTYVAPSTVDSIKXEGSPQPKLRSPRLNSPR 424

RESULT 8
 US-09-925-298-663
 ; Sequence 663, Application US/09925298
 ; Publication No. US20020039764A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: PA103
 ; CURRENT APPLICATION NUMBER: US/09/925,298
 ; CURRENT FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 846
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 663
 ; LENGTH: 272
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; NAME/KEY: SITE
 ; LOCATION: (129)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; US-09-925-298-663

Query Match 49.8%; Score 1303; DB 12; Length 272;
 Best Local Similarity 99.6%; Pred. No. 7.7e-86;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 253 ILVRSGNRAVDWMSIGALMYDMLTGSPPTABNRKTMMDKIRGLALPVLTPDARLV 312
 DB 30 ILVRSGNRAVDWMSIGALMYDMLTGSPPTABNRKTMMDKIRGLALPVLTPDARLV 89
 QY 313 VKKFLKSNPSQIRIGGPGDAADVQRRPFRHNMDLAWRVDPFRPPCLQSEEDVSOQD 372
 DB 90 VKKFLKSNPSQIRIGGPGDAADVQRRPFRHNMDLAWRVDPFRPPCLQSEEDVSOQD 149
 QY 373 TRFTRQTPVDSDDPDLSSANQALGFTYVAPSTVDSIKXEGSPQPKLRSPRLNSPR 432
 DB 150 TRFTRQTPVDSDDPDLSSANQALGFTYVAPSTVDSIKXEGSPQPKLRSPRLNSPR 209
 QY 433 VPVSPFLKSPFEGGRSPSPSPPTLPLPPLPPTSTAPLPIRPPSGTKSKRGGR 492
 DB 210 VPVSPFLKSPFEGGRSPSPSPPTLPLPPLPPTSTAPLPIRPPSGTKSKRGGR 269
 QY 493 PGR 495
 DB 270 PGR 272

QY 425 BRUNSSRVVSPKESP--FEGRRSPSPLEPELPLPPPPS-----470
 DB 253 RRTIGSRIVSPKESBDFWKGASAS---TANQOTVEYMETSGIGMDVTMSGE 308
 QY 471 TTAPLPIRP-SGTRSK 487
 DB 309 ASAPLPIRPNRSGYKKQ 326

RESULT 12
 US-10-108-260A-3334
 ; Sequence 3334, Application US/10108260A
 ; Publication No. US20040005560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HELIX RESEARCH INSTITUTE
 ; TITLE OF INVENTION: No. US20040005560A1 full length cDNA
 ; FILE REFERENCE: HI-A0106
 ; CURRENT APPLICATION NUMBER: US/10/108,260A
 ; CURRENT FILING DATE: 2002-03-27
 ; NUMBER OF SEQ ID NOS: 5458
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3334
 ; LENGTH: 544
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 ; US-10-108-260A-3334

Query Match 36.4%; Score 955.5; DB 15; Length 544;
 Best Local Similarity 45.8%; Pred. No. 1,86-60;
 Matches 196; Conservative 74; Mismatches 105; Indels 53; Gaps 9;

QY 43 PLALB---RAAGLEPVGHYEVELTETSVA--VGP-----72
 DB 2 PIQOLELMWKIEVEPW---ELETSEBDNLDPGATBDTAESEGVKZEIDISHNVK 57
 QY 73 --BRIGPHCELLRVYKGGYGVFOYRKVQGTNIGKIYAMKYLAKAKIYRNADKPTAHR 130
 DB 58 GFKRAPSQBELKLVQSSYGVFLVRKVGSDAQGLYAMKYLAKATL--KYRDRVRK 115
 QY 131 AERNIIEVYKPIYELAVAFQTKGLYLLIECLSGSELFTHLEREGIFLEDTACFYLA 190
 DB 116 MERDIIAEVNHPIVKLHYAFQTEGSKLYLLIDPLRGGDLFTRLSKVEMFTSEDVKFLAB 175
 QY 191 ITALGLHSOGIYYIDKPEINMLSSQGHIXLTDGLCESEIHGAVHTPQGTIEVNA 250
 DB 176 IALALDLHSLGIYIDKPEINMLLDEGHIXITDRLSEKALIDHDKRAVSFGTIEVNA 235
 QY 251 PELIVSGNRAVDWMSIGALMYDMLTGPPTAENRKKIMDKIRGKUALPPYLTPDAR 310
 DB 236 PEVYVNRGHTQSDAMWSFVLMFEMLGLPFGQKDKRKMALILKAKLGMFGLSGEAQ 295
 QY 311 DYVKKFLKRPQRIIGGSGDADVDQRRPFRHMMDDLLAMVDPFRCLQSEEDVQ 370
 DB 296 SLIRALFKRNPCKRLGAGIDGVEIRKHPFVTIDMTWTLRKIKPFPKAVGPRPDTH 355
 QY 371 FDRFTSQTPVSDPDALSESANQAFLGTYVAPSVLDSIKGFSFOPLASPRILNS 430
 DB 356 FDEFTARTPTDSE--GVPRSMNHILFRGSSFVASSLIDQ-----EP---SQGLH-- 401
 QY 431 PRVPSPL 438
 DB 402 -KVPVHPI 408

RESULT 13
 US-10-369-493-5149
 ; Sequence 5149, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.

APPLICANT: Goldman, Barry S.
 TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
 FILE REFERENCE: 38-10(52052)B
 CURRENT APPLICATION NUMBER: US/10/369,493
 CURRENT FILING DATE: 2003-02-28
 PRIOR APPLICATION NUMBER: US 60/360,039
 PRIOR FILING DATE: 2002-02-21
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 5149
 LENGTH: 740
 TYPE: PRF
 ORGANISM: Caenorhabditis elegans
 US-10-369-493-5149

Query Match 36.4%; Score 951.5; DB 15; Length 740;
 Best Local Similarity 47.9%; Pred. No. 5,16-60;
 Matches 190; Conservative 69; Mismatches 105; Indels 33; Gaps 5;

QY 23 ETEEGSGEPELSPADACPLAEPLAAGLEPVGHYEVELTETSVA--BRIGP 77
 DB 6 EYEFRAENIEGGEBKTDSS-----SETEIDIGVAKCKEADP 44
 QY 78 HCEPLRLVYKGGYGVFOYRKVQGTNIGKIYAMKYLAKAKIYRNADKPTAHRNILE 137
 DB 45 ROPELLKVLQSSYGVFLVRKVRGDSGHVYAMKYLAKATL--KYRDRQTKERNILA 102
 QY 138 SVKPFPIYELAVAFQTKGLYLLIECLSGSELFTHLEREGIFLEDTACFYLAITLALGH 197
 DB 103 HSHFPIYKLAHAFTEBKLYLLIDPLRGGDLFTLSKVMFTSEDVKFLAEFLTALH 162
 QY 198 LHSQGIYIDKPEINMLSSQGHIXLTDGLCKESIHBGAVHTPQGTIEVNAPEILVRS 257
 DB 163 LHSIIDIYVDLKPENILDAQGIKVTDFGLSKEDIBSKKYSFGVGVYAPVINKR 222
 QY 256 GGNRAVDWMSIGALMYDMLTGPPTAENRKKIMDKIRGKUALPPYLTPDARIVKFL 317
 DB 222 GHSMAADRLSLGLVLMFEMLGLPFGQKDRDITMQLKAKLSMHPFLQEAQSLRALF 282
 QY 318 KNPQRIIGGSGDADVDQRRPFRHMMDDLLAMVDPFRCLQSEEDVQSPOTRFT 377
 DB 283 KNSQNRKLGAGIDGVEIRKHPFVTIDMTWTLRKIKPFPKAVGPRPDTH 355
 QY 378 QTPVSDPDALSESAN--QAFVLTGYVAPSVLDSIK 412
 DB 343 RPKDSP---ALPASANGHILFRGSSFVASSVAMEERK 376

RESULT 14
 US-09-771-161A-265
 ; Sequence 265, Application US/09771161A
 ; Patent No. US20020110811A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LEVINE, et al.
 ; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
 ; FILE REFERENCE: 802620-2005.1
 ; CURRENT APPLICATION NUMBER: US/09/771,161A
 ; CURRENT FILING DATE: 2001-01-26
 ; PRIOR APPLICATION NUMBER: 09/724,676
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 136776
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 135619
 ; PRIOR FILING DATE: 2000-04-12
 ; NUMBER OF SEQ ID NOS: 273
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 265
 ; LENGTH: 740
 ; TYPE: PRF
 ; ORGANISM: Homo sapiens
 ; US-09-771-161A-265

Query Match 36.3%; Score 949.5; DB 9; Length 740;
 Best Local Similarity 48.7%; Pred. No. 7.1e-60;
 Matches 185; Conservative 65; Mismatches 105; Indels 25; Gaps 4;

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QY 29 EGGEPELSPADACIALRAAGLEPVGHTEVELTETS---VNVGERIGPHCELLR 84
DB 31 EPMGEERINP-----QTEBVSIKELAITHHVKEGHEKADPSQFELK 72
QY 85 VLGGKGYKVFQVRKVGSTNLGIYAMKVLKRAKIVRNADTAFTRAERNILLESVKHPFI 144
DB 73 VLGGGSFGKVFVLYKKISGSDARQLYAMKVLKATL--KYRDRVATKMERDILVEVNHPI 130
QY 145 VELAYAFQTGKLYLILECLSGELFTHLERBGIFLEDTACFYLAETTLAIGHLSGII 204
DB 131 VKLHYAFQTGKLYLILDFIRGGLFTPLSKKVFTEEDVVFYLAIALADHLHSIGII 190
QY 205 YRDLKPEINIMLSQGHKLTDFGLCKESIHEGAVTHTECGTIEYMADEILVRSGNRAVD 264
DB 191 YRDLKPEINILDEBGIKLTDFGLSKESIDHEKAYSCGIVEYMADEVNRGHQSAD 250
QY 265 WWSLGALMYDMLTGSPPETAENRKTMDKIIKGLALPYLTDPARDLVKKFLKRNPSOR 324
DB 251 WWSFGVLMFEMLTGLTFQGRKREITWMLKALGMFQFLSPAQSILMLFKRNPNR 310
QY 325 IGGPGDAADVORHPFRHMMWDDLAMRYDPPFRPCLQSEEDVSCQDERFTTQTPYDSP 384
DB 311 LGAGPDGVEEIKKHSFSTIDMKLYRREIHPKPAATGRPEDTFFPDPEPTAKTPDPS 370
QY 385 DDTALSESANQAFLGFTYVA 404
DB 371 -GIPPSANAHQLFRGFSFVA 389

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RESULT 15

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US-09-771-161A-266
; Sequence 266, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771.161A
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 266
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-266

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Query Match 36.3%; Score 949.5; DB 9; Length 740;
 Best Local Similarity 48.7%; Pred. No. 7.1e-60;
 Matches 185; Conservative 65; Mismatches 105; Indels 25; Gaps 4;

```

QY 29 EGGEPELSPADACIALRAAGLEPVGHTEVELTETS---VNVGERIGPHCELLR 84
DB 31 EPMGEERINP-----QTEBVSIKELAITHHVKEGHEKADPSQFELK 72
QY 85 VLGGKGYKVFQVRKVGSTNLGIYAMKVLKRAKIVRNADTAFTRAERNILLESVKHPFI 144
DB 73 VLGGGSFGKVFVLYKKISGSDARQLYAMKVLKATL--KYRDRVATKMERDILVEVNHPI 130
QY 145 VELAYAFQTGKLYLILECLSGELFTHLERBGIFLEDTACFYLAETTLAIGHLSGII 204
DB 131 VKLHYAFQTGKLYLILDFIRGGLFTPLSKKVFTEEDVVFYLAIALADHLHSIGII 190

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QY 205 YRDLKPEINIMLSQGHKLTDFGLCKESIHEGAVTHTECGTIEYMADEILVRSGNRAVD 264
DB 191 YRDLKPEINILDEBGIKLTDFGLSKESIDHEKAYSCGIVEYMADEVNRGHQSAD 250
QY 265 WWSLGALMYDMLTGSPPETAENRKTMDKIIKGLALPYLTDPARDLVKKFLKRNPSOR 324
DB 251 WWSFGVLMFEMLTGLTFQGRKREITWMLKALGMFQFLSPAQSILMLFKRNPNR 310
QY 325 IGGPGDAADVORHPFRHMMWDDLAMRYDPPFRPCLQSEEDVSCQDERFTTQTPYDSP 384
DB 311 LGAGPDGVEEIKKHSFSTIDMKLYRREIHPKPAATGRPEDTFFPDPEPTAKTPDPS 370
QY 385 DDTALSESANQAFLGFTYVA 404
DB 371 -GIPPSANAHQLFRGFSFVA 389

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Search completed: June 30, 2004, 17:20:18
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OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)

3612.682 Million cell updates/sec

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Perfect score: 2614
Sequence: 1 MARGRRRAGGAAMAAVFDL.....PIRPPSGTKKSKKRGRRGRR 495

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Delop 6.0, Delext 7.0

Searched: 3163042 seqs, 2412103600 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1	2596	99.3	1742	13	US-10-425-114-18480	Sequence 18480, A
2	1947.5	74.5	1637	10	US-09-968-433-10	Sequence 10, Appl
3	1748	66.9	2236	9	US-09-954-156-1137	Sequence 1137, Ap
4	1748	66.9	2346	10	US-09-920-677-3	Sequence 3, Appl
5	1748	66.9	2346	13	US-10-388-360-321	Sequence 321, Appl
6	1746	66.8	1800	15	US-10-316-253-31	Sequence 31, Appl
7	1740	66.6	2287	15	US-10-316-253-33	Sequence 33, Appl
8	1740	66.6	2287	16	US-10-191-803-230	Sequence 230, Appl
9	1724.5	66.0	2362	13	US-10-425-114-26874	Sequence 26874, A
10	1646	63.0	1197	13	US-09-925-289-245	Sequence 245, App
11	1646	63.0	1197	15	US-10-102-806-245	Sequence 245, App
12	1455	55.7	2556	9	US-09-817-310-1	Sequence 1, Appl
13	1406.5	53.8	1058	10	US-09-968-433-58	Sequence 58, Appl
14	1385.5	53.0	1607	16	US-10-305-720-146	Sequence 120, Appl
15	1211.5	46.3	843	13	US-10-220-955-1	Sequence 1, Appl
16	980.5	37.5	3206	16	US-10-159-553-155	Sequence 155, App
17	966	37.0	3061	9	US-09-880-107-2146	Sequence 2146, Ap
18	958	36.6	3673	15	US-10-240-965-2146	Sequence 2146, Ap
19	955.5	36.6	4098	16	US-10-108-260A-891	Sequence 891, App
20	942	36.0	669	16	US-10-305-720-118	Sequence 118, App
21	937.5	35.9	2403	15	US-10-102-554-1	Sequence 1, Appl
22	910.5	34.8	3169	13	US-10-425-114-26242	Sequence 26242, A
23	907.5	34.7	4563	14	US-10-002-600-14	Sequence 14, Appl
24	886.5	33.9	3131	13	US-10-342-887-972	Sequence 972, App
25	886.5	33.9	3131	13	US-10-172-118-972	Sequence 972, App
26	856	32.7	3120	15	US-10-112-286-1	Sequence 1, Appl
27	851.5	32.6	1666	13	US-10-424-559-34191	Sequence 34191, A
28	850.5	32.5	1440	13	US-10-425-114-7797	Sequence 7797, Ap
29	850	32.5	491	10	US-09-968-433-57	Sequence 57, Appl
30	844	32.3	594	13	US-10-240-315-2	Sequence 2, Appl
31	824	31.5	1335	16	US-10-116-275-285	Sequence 285, App
32	813.5	31.1	673	9	US-09-925-300-418	Sequence 418, App
33	810.5	31.0	1315	13	US-10-403-161-3	Sequence 3, Appl
34	810.5	31.0	1388	15	US-10-067-977-1	Sequence 1, Appl
35	810.5	31.0	2281	16	US-10-131-410-39	Sequence 39, Appl
36	810.5	31.0	2343	13	US-10-403-161-1	Sequence 1, Appl
37	810.5	31.0	2354	15	US-10-210-120-22	Sequence 22, Appl
38	810.5	31.0	2265	9	US-09-981-355-6	Sequence 6, Appl
39	810.5	31.0	3196	16	US-10-094-749-222	Sequence 222, App
40	807	30.9	2025	17	US-10-437-963-73382	Sequence 73382, A
41	806.5	30.9	2370	9	US-09-969-347-214	Sequence 214, App
42	806.5	30.9	2370	9	US-09-880-107-3855	Sequence 3855, Ap
43	806.5	30.9	2370	15	US-10-000-039-1	Sequence 1, Appl
44	806.5	30.9	2370	16	US-10-353-690-11	Sequence 11, Appl
45	804	30.8	1308	16	US-10-368-493-46340	Sequence 46340, A

ALIGNMENTS

RESULT 1
US-10-425-114-18480
Sequence 18480, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jindong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B.
APPLICANT: Tabaka, Jack B.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 18480
LENGTH: 1742
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Clone ID: LTB3081-101-B10_FLI


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QY 1 MetAlaArgGlyAArgAlaArgGlyAlaGlyAlaAla----- 13
Db 28 ATAGAGCGAAGAGAGAGCGGACGGCTTTTACCACGCCCGGACCTTCCGAGACAGGAA 87
QY 14 -----MetAlaAlaValPheAspLeuAspLeuGluThrGluGluSerGluGly 30
Db 88 GCTGAGGACATGGCAGAGAGGTGTTGACATGACCTTGACCGACAGACGCGGGCTCT 147
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49
Db 148 GAGGATGAGCTGAGG-----GAGGGGGCTCAGTTTAAATGAAAGCATGAGCAAT 195
QY 50 AlaGlyLeuGluPro-----ValGlyHisTyrGluGluGluValGluLeuThrGlu 65
Db 196 GGGGAGGTGACCATATGAACTTGGCAGTGAACATTTGAGAAATTTGAATCTCAGAA 255
QY 66 ThrSerValAsnValGlyProGluArgGlyGlyProHisCysPheGluLeuLeuAlaGly 85
Db 256 ACTAGTGTGAACAGAGGCGGAAATAATGACAGCAAGATGTTTGAAGCTACTTCCGGTA 315
QY 85 LeuGlyLysGlyGlyTyrGlyLysValPheGluValArgLysValGluGlyThrAsnLeu 105
Db 316 CTGGTAAAGGGGCTATGGAAGGTTTTCAGAGTACGAAAGTAAAGAGAGCAATACT 375
QY 106 GlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAlaAlaLysAsp 125
Db 376 GCGAAATATATTTCCCATGAAGGTCTTAAAGGCAATGATGTAAGAAATGCTAAAGAT 435
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleVal 145
Db 436 ACAGCTCATACAAAGCAAGAGCAAGATTTCTGAGAGAGTAAAGATCCCTTCATCGTG 495
QY 146 GluLeuAlaTyrAlaPheGluThrGlyLysLeuTyrLeuIleLeuGluCysLeuSer 165
Db 496 GATTATATTATTCCTTTCAGATCGTGTGAAACCTTACCTCATCTTGAAGTATCTCAGT 555
QY 166 GlyGlyGluLeuPheThrHisLeuGluArgGlyLysPheLeuGluAspThrAlaCys 185
Db 556 GAGAGGAACTATTATTCAGATTCAGAAAGAGGAAATTTATGGAAGACGTGCTGCTGC 615
QY 186 PheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleTyr 205
Db 616 TTTTACTGTCGACAAATCTCCATGCTTTGGGGCATTTTCACTCAAAAGGGATCATCTAC 675
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisIleLeuLeuThrAsp 225
Db 676 AGAGACTTAAGCGGAGATATCATGCTTAATCACCAAGGTCATGTGAACCTTAACAGAC 735
QY 226 PheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThr 245
Db 736 TTTGACATATGCAAAAGATCATATTCATATGGAAGACGTACACACACATTTTGTGAAACA 795
QY 246 IleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyr 265
Db 796 ATAGAAATACATGCCCCCTGAAATCTTGATGAGAAAGGCGCAACATCGTCTGTGATGG 855
QY 266 TrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGlu 285
Db 856 TGGAGTTTGGAGCATTAATGATATGACATGCTGACGAGACACCCCATCTGCTGGAGAG 915
QY 286 AsnArgLysLysThrMetCysLysIleIleArgGlyLysLeuAlaLeuProTyrLeu 305
Db 916 AATAGAAAGAAACAAATGACAAATCTCAATGTAATCAATTTGCTCCCTACCTC 975
QY 306 ThrProAspAlaArgAspLeuValLysPheLeuLysArgAsnProSerGluThrGly 325
Db 976 ACACAGAGAGCCAGAGATCTGCTTAAGAGCTGCTAAAGAAATGCTCTGCTGCTG 1035
QY 326 GlyGlyGlyProGlyAspAlaAlaAspValGluArgHisProPhePheArgHisMetAsn 345
Db 1036 GAGAGCTGCTCGGGACCTCGAGAGAGTCAAGCTCATCCATCTTTTGAACACATTAAC 1095
QY 346 TrpAspAspLeuLeuAlaTrpArgValAspProProPheArgProCysLeuGluSerGlu 365

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Db 1096 TGGGAGAACTTCTGCTCGAAGGTGAGGCCCTTTAACTCTGTGTGACATCTGA 1155
QY 366 GluAspValSerGluPheAspThrArgPheThrArgGluThrProValAspSerProAsp 385
Db 1156 GAGGATGTAAAGTCACTTGATTTCCAACTTTCACCTCAGACACCTGTGACAGCCAGAT 1215
QY 386 AspThrAlaLeuSerGluSerAlaAsnGluAlaPheLeuGlyPheThrTyrValAlaPro 405
Db 1216 GACTCAACTCATAGGAAAGTCCCAATCAAGCTTTCTGCGTTTACATATGCTCTCA 1275
QY 406 SerValLeuAspSerIleLysGluGlyPheSerPheGluProLysLeuArgSerProArg 425
Db 1276 TCTGTACTTGAAGAGTGAAAGAAAGTTTCTTGTGAACCAAAATCGATCACTTCA 1335
QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe 443
Db 1336 AGATTTATTTGGAGCCACAGACACCTGTGACGCCACGATCAATTTTCTCTGGGATTTTC 1395
QY 444 GluGlyPheArgProSerProSerLeuProGluProThrGluLeuProLeuProLeu 463
Db 1396 TGGGAGAGAGGTCTTCCGCGCAGC-----ACAGCAATCTCAGACACCTGTG 1443
QY 464 LeuProProProProProSer-----Thr 471
Db 1444 GAAATCCCAATGAGAAACAAAGTGGCATGACAGATGATGTGACATGATGGGAGAGCA 1503
QY 472 ThrAlaProLeuProIleArgProProSerGlyThrLys----- 484
Db 1504 TCGGACACACTTCCAAATGACAGCGCAACTCTGGGCAATACAAAGAAAGCTTTTCCC 1563
QY 484 ----- 484
Db 1564 ATGATCTCCAAACGGCCAGAGCACCTGGGTATGAAATCTATGACAGAGCAATGCTTTAAT 1623
QY 485 -----LysSerLysArgGlyArgGlyArg 492
Db 1624 GAATTTAAGCAAAAGGTGAGAGAGGAGA 1653

RESULT 4
US-09-920-677-3
/ Sequence 3, Application US/09920677
/ Publication No. US2003083284A1
/ GENERAL INFORMATION:
/ APPLICANT: Brett P. Monia
/ TITLE OF INVENTION: ANTISENSE MODULATION OF P70 S6 KINASE EXPRESSION
/ FILE REFERENCE: RTS-0245
/ CURRENT APPLICATION NUMBER: US/09/920,677
/ CURRENT FILING DATE: 2001-08-01
/ NUMBER OF SEQ ID NOS: 49
/ SEQ ID NO 3
/ LENGTH: 2346
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURES:
/ NAME/KEY: CDS
/ LOCATION: (28) ... (1605)
US-09-920-677-3

Alignment Scores:
Pred. No.: 1,04e-167 Length: 2346
Score: 1748.00 Matches: 354
Percent Similarity: 73.45% Conservative: 50
Best Local Similarity: 64.36% Mismatches: 80
Query Match: 66.87% Indels: 66
DB: 10 Gaps: 8

US-09-762-258-2 (1-495) x US-09-920-677-3 (1-2346)
QY 1 MetAlaArgGlyAArgAlaArgGlyAlaGlyAlaAla----- 13
Db 28 ATAGAGCGAAGAGAGAGCGGACGGCTTTTACCACGCCCGGACCTTCCGAGACAGGAA 87

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QY 14 -----MetAlaValIlePheAspLeuAspLeuThrGluGluGlySerGluGly 30
Db GGTGAGACATGGCGAGTGTGTTGACATGACCTGACACCGACGAGGAGCTCT 147
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49
Db GAGATGAGCTGGAG-----GAGGGGGCTCAGTTTAATGAAAGCATTGACCAT 195
QY 50 AlaGlyLeuGluPro-----ValGlyHisTyrGluGluValAlaGluLeuThrGlu 65
Db GGGGAGGTGACCATATGAACTTGGCATGAAACATTGAGAAATTTGAATCTCAGAA 255
QY 66 ThrSerValAsnValGlyProGluArgGlyLeuGlyProHisCysPheGluLeuLeuArgVal 85
Db ACTAGTGTGAACGAGGGCCGAAAAAATCAGACCAAGAAATTTTGAAGCTTCTCGGGTA 315
QY 86 LeuGlyLysGlyGlyTyrGlyLysValPheGluValAlaGlyValGluGlyThrAspLeu 105
Db CTGGTAAAGGGGCTATGGAAGCTTTTCAAGTACAAAAGTAAAGCAAGCAAAATCT 375
QY 106 GlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValArgAsnAlaLysAsp 125
Db GGGAAAAATTTGCTCAAGAGTGTCTTAAAGGCAATGATGTAAGAAATGCTAAAGAT 435
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValLysHisProPheIleVal 145
Db ACAAGCTACAAAAGCAAGCAAGCAATTTCTGAGAGAAAGTAAAGCAATCCCTCATCTG 495
QY 146 GluLeuValaTyrAlaPheGluThrGlyGlyLysLeuTyrLeuIleLeuGluCysLeuSer 165
Db GATTAAATTTATGCTTTCAGACTGTGAAAGCACTCACTCATCTGATATCTCAGT 555
QY 166 GlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
Db GAGAGAGAACTATTATGCAAGTAAAGAGAGAAATATTATGAGAAAGACATGCTGCTC 615
QY 186 PheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleTyr 205
Db TTTACTTGGCAGAAATCTCATGCTTGGGCAATTACATCAAAAGGGATCATCTAC 675
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisIleLysLeuThrAsp 225
Db AGAAGCTGGAAGCGGAGAAATATCATGCTTAAACCAAGCTGAGAACTTAACAGAC 735
QY 226 PheGlyLeuCysLysGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThr 245
Db TTTGAGCTATGCAAGATCTATTCATCATGAGAACATGACACACATTTTGTGGAAAC 795
QY 246 IleGluTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyr 265
Db ATAAAGAAATACATGCGCCCTGAAATTTGATGAGAAAGTGGCCCAATCTGCTGCAATGG 855
QY 266 TyrSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPhePheThrAlaGlu 285
Db TGGAGTTTGGAGCATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 915
QY 286 AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeu 305
Db AATGAGAAAGAAACAAATTTGACAAATCTCAATATGTAATCAATTTGCTCCCTACCTC 975
QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGluAspIle 325
Db ACACAAAGAGCCAGAGATCTGCTTAAAGCTGTGAAAGAAATGCTGCTCTGCTGCTG 1035
QY 326 GlyGlyGlyProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsn 345
Db GGAAGCTGCTCTGGGAGAGCTGAGAGAAATTCAGAGCTCATCTCTTAAACACATTAAC 1095
QY 346 ThrAspAspLeuLeuAlaTyrArgValAspProPheArgProCysLeuGluInserGlu 365
Db TGGAGAAATCTTCTGGCTGAAAGTGGAGCCCTTTTAAACCTTGTTGCAATCTGAA 1155

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QY 366 GluAspValSerGluInPheAspThrArgPheThrArgGluInThrProValAspSerProAsp 385
Db GAGATGTAATCACTAGTTGATTTGATTCAGATTACAGTACAGACCTGTCGACAGCCAGAT 1215
QY 386 AspThrAlaLeuSerArgLysSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaPro 405
Db GACTCAACTCTCAATGAAAGTGGCAATCAGGCTTTCTGGGTTTAAATATGTGGCTTCA 1275
QY 406 SerValLeuAspSerIleLysGluGlyPheSerPheGluInProLysLeuArgSerProArg 425
Db TCTGATCTGTAAGATGTGAAAGAAAGATTTTCTTTGACCAAAAATCCGATCACTCGA 1335
QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerPro-----Phe 443
Db AGATTATTTGGCAGCCCAACAAACACCTGTGAGCCCACTCAAAATTTTCTCTGGGGATTC 1395
QY 444 GluGlyPheArgProSerProSerProLeuProGluProThrGluLeuProLeuProLeu 463
Db TGGGAAAGAGTGTCTTGGCCAGC-----ACAGCAATCTCTCAGACACTGTG 1443
QY 464 LeuProProProProProSer-----Thr 471
Db GAATACCCCAATGAAACAAAGTGCATGACAGATGATGACATGATGACATGATGAGGAGCA 1503
QY 472 ThrAlaProLeuProIleArgProProSerGlyThrLys----- 484
Db TGGCAGCACTTCCATACAGACAGCCAGACTCTGGGCGCATACAAAACAAAGCTTTCCC 1563
QY 484 ----- 484
Db ATGATCTCAAGCGCAGACACCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1623
QY 485 -----LysSerLysArgGlyArgGlyArg 492
Db GAATTTAAGGCAAAAGGTGAGAGGAGGA 1653

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RESULT 5

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US-10-388-360-321
; Sequence 321, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Jofire B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OR INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCES: 39740-00010US
; CURRENT APPLICATION NUMBER: US/10/388,360
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-321
Alignment Scores:
Pred. No.: 1,046-167
Score: 1748.00
Percent Similarity: 73.45%
Best Local Similarity: 64.36%
Query Match: 66.87%
DB: 13
Length: 2346
Matches: 354
Conservative: 50
Indels: 66
Gaps: 8

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US-09-762-258-2 (1-495) x US-10-388-360-321 (1-2346)

DB: 15 Gaps: 7

US-09-762-258-2 (1-495) x US-10-316-253-31 (1-1800)

QY 14 MetAlaValAlaPheAspLeuAspLeuThrGluGluGlySerGluGluGlyGlu 33

DB 134 ATGGAGGAGGTGGTGGATGACCTGGAGCCGAGGATGAGGCTTGAAGATGAG 193

QY 34 ProGluSerProAlaAspAlaCysProLeuAlaGlu--LeuArgAlaAlaGlyLeu 52

DB 194 CTGAGG-----GAGGGGGGTGAGTTAAATGAAAGCAATGAGCAATGGGGAGTT 241

QY 53 GluPro-----ValGlyHisTyrGluGluValGluLeuThrGluThrSerVal 68

DB 242 GGACCATATGAACTTGGCATGGAACATTGTGAGAAATTTGAAATCTGAGAACTAGGTG 301

QY 69 AsnValGlyProGluArgGlyGlyProHisCysPheGluLeuLeuArgValLeuGlyLeu 88

DB 302 AACAGAGGCGCAAAAATATGACCAAGATGTTTGGCTACTTGGGTACTTGTAA 361

QY 89 GlyGlyTyrGlyLeuValPheGluValArgGlyValGluGlyThrAsnLeuGlyLeu 108

DB 362 GGGGGCTATGAAAGGTTTTCAGTACGAAAGTAACAGAGCAAAATATCTGGGAGATA 421

QY 109 TyrAlaLeuValLeuArgValAlaValSerHisArgAsnAlaValAspThrAlaHis 128

DB 422 TTTCCTATGAGGTGCTTAAAGCAATGATGATGAAATGCTTAAAGATACAGCTCAT 481

QY 129 ThrArgAlaGluArgAsnLeuGluSerValIshHisProPheIleValGluLeuAla 148

DB 482 ACAAAACAGAGCGGAATATTCTGAGAGAAATGAAACATCCCTTCATCGAGATTATAT 541

QY 149 TyrAlaPheGluThrGlyGlyLeuLeuTyrLeuLeuGluGlyCysLeuSerGlyGlyGlu 168

DB 542 TATGCTTTTACAGCCGGTGAAGAACTTACTCATCTTGAATATCTCAGCTGAGAGAA 601

QY 169 LeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCysPheTyrLeu 188

DB 602 CTATTATGACAGTTAAGAGAGAGGGATATTCATGAGAAAGTACAGCTCTTCTTACTTG 661

QY 189 AlaGluLeuThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleIleTyrArgAspLeu 208

DB 662 GCTGAATATCTCAGAGGCTTGGGGCATTTTCATTAATAAAGAGATCATCTACAGAGCTG 721

QY 209 LysProGluAsnIleMetLeuSerSerGlyGlyHisIleLeuLeuThrAspPheGlyLeu 228

DB 722 AAGCCGAGAACATCATGCTTAATACCAAGTCACCTGAGAGCTGAGACTTGGACTA 781

QY 229 CysIleGluSerIleHisGluGlyAlaValThrHisThrPheCysGlyThrIleGluTyr 248

DB 782 TGCMAAAGATCTATTCTATGATGAAACAGTCACGACACATTTGTGMAACAATAGATAC 841

QY 249 MetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspThrIlePheSerLeu 268

DB 842 ATGCCCCCTGAATCTTATGATGAGAGAGCCACACAGCTGTGAGATGAGTGGAGTTTG 901

QY 269 GlyAlaLeuMetTyrAspMetLeuThrGlySerProPheThrAlaGluAsnArgGlyLeu 288

DB 902 GGAGCATTAATGATGATCATGCTGATGAGACCTTCATTCCTGGGAGGAAATAGAAAG 961

QY 289 LysThrMetAspIleIleIleArgGlyLeuLeuAlaLeuProTyrLeuThrProAsp 308

DB 962 AAAACAAATTAACAAATCTCAATGTAATCTTAATTTGCTCCCTACCTACCAAGAA 1021

QY 309 AlaArgAspLeuValIshPheLeuValArgAsnProSerGluArgIleGlyGlyGly 328

DB 1022 GCTCGAGATCTGCTTAAAGAGCTGCTGAAAGAAAGAGAGCTCTGCTGTGAGAGCTGG 1081

QY 329 ProGlyAspAlaAlaAspValGlnArgHisProPhePheArgHisMetAsnTyrAspAsp 348

DB 1082 CTGGGGATGCTGGAGAGGTCCAAAGCGCATCTTTTATGACACATTAATCTGGAGAGAG 1141

QY 349 IleuLeuAlaTyrArgValAspProProPheArgProCysLeuGluSerGluAlaVal 368

DB 1142 CTTTGGCTCGAAGGTGAGAGCCCTTTAAGCTCTGTGCAATCTGAAGAGATGTG 1201

QY 369 SerGluPheAspThrArgPheThrArgGluThrProValAspSerProAspAspThrAla 388

DB 1202 AGTCAATTAATTAATCAAGTTTACTCGTCACACCTGTGTACAGCCCCGATGACTCACT 1261

QY 389 LeuSerGluSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaProSerValLeu 408

DB 1262 CTCAGTAAAGTGCACCAACAGAGCTTCTGCTGTTTATCATATATGGCTCATCTGTACTT 1321

QY 409 AspSerIleLeuGluGlyPheSerPheGluProLysLeuArgSerProAlaGlyLeuAsn 428

DB 1322 GAAAGGTGTAAGAAAGATTTTCTTTTGAACCAAAATCGATCGCTCCAGATTTAT 1381

QY 429 SerSerProArgValProValSerProLeuLysPheSerProPheGlu----- 444

DB 1382 GGTAGCCCAAGAACGCTGTGACCCCAAGTAAATTTCTCTCGGATTTCTGGAGCA 1441

QY 445 GlyPheArgProSerProSerLeuProGlu--ProThrGluLeuProLeuProLeu 463

DB 1442 GGTGCTTACAGCCAGACAGCAAAATCCTCAGACACCTGTGAAATACCAATGAAACAGT 1501

QY 464 LeuProProProProProSerThrThr-----AlaProLeuProIleArg 478

DB 1502 GGAATGAGACAGATGATGTGACACAGAGGGGAAAGCTTCAGGCGCATTCATCCGA 1561

QY 479 ProPro--SerGlyThrIshSerLys 487

DB 1562 CAGCCCACTCTGGCCATTAACAAACAA 1591

RESULT 7

US-10-316-253-33

Sequence 33, Application US/10316253

Publication No. US20030162706A1

GENERAL INFORMATION:

APPLICANT: The Procter & Gamble Company

APPLICANT: Peters, Kevin

APPLICANT: Thompson, Larry

APPLICANT: Meng, Feng

APPLICANT: Greis, Kenneth

TITLE OF INVENTION: Angiogenesis Modulating Proteins

FILE REFERENCE: 8865M

CURRENT APPLICATION NUMBER: US/10/316,253

PRIOR FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: US 60/355,295

PRIOR FILING DATE: 2002-02-08

NUMBER OF SEQ ID NOS: 308

SOFTWARE: PatentIn version 3.1

SEQ ID NO 33

LENGTH: 2287

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURE:

NAME/KEY: CDS

LOCATION: (22) .. (1599)

OTHER INFORMATION:

US-10-316-253-33

Alignment Scores:

Prod. No.: 6,54E-167 Length: 2287

Score: 1740.00 Matches: 349

Percent Similarity: 77.97% Conserved: 51

Best Local Similarity: 68.03% Mismatches: 83

Query Match: 66.56% Indels: 30

DB: 15 Gaps: 8

US-09-762-258-2 (1-495) x US-10-316-253-33 (1-2287)

QY 1 MetAlaArgGlyArgArgAlaArgGlyAlaGlyAla----- 13

DB 22 ATGAGCGCAGCAGCAGAGGGGAGCGCTTTTACCAAGCGCTTACCTTCAGACAGAGGAA 81

QY 14 -----MetAlaValPheAspLeuAspLeuThrGluGluGlySerGluGly 30
 DB 82 GCTGAGGACATGGCAGAGTGTGATGACCTGGACGACGACGATGAGGCTCT 141
 QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu--LeuArgAla 49
 DB 142 GAGGATGAGCTGGAG-----GAGGGGGGTCACTTAATGAAAGCATGACCAT 189
 QY 50 AlGlyLeuGluPro-----ValGlyHisTyrGluGluValGluLeuThrGlu 65
 DB 190 GGGGGGCTTGACCATATGAACTTGGCATGAACTTGGAGAAATTTGAAATCTCGAA 249
 QY 66 ThrSerValAsnValGlyProGluArgGlyIleGlyProHisCysPheGluLeuLeuArgVal 85
 DB 250 ACTAGGTGTAACAGAGGGCCAGAAAATAACAGACCGAAGTGTTTAGAGCTACTGGGTA 309
 QY 86 LeuGlyGlyGlyGlyGlyGlyValPheGluValArgGlyValGluGlyThrAsnLeu 105
 DB 310 CTGGTAAAGGGGGCTATGAAAGGTTTCAAGTACGAAAGTAAACAGAGCAATTAAT 369
 QY 106 GlyValIleTyrAlaMetLysValLeuArgGlyAlaIleValArgAsnAlaLysAsp 125
 DB 370 GGGAGATATTTCCATGAAAGTGTCTTAAAGGCAATGATAGTAAAGATGCTAAAGAT 429
 QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValIleHisProPheIleVal 145
 DB 430 ACAGCTCATCAAAAGAGAGCGGAATATCTGAGAGAAATTAAGCATCCCTTCATTGG 489
 QY 146 GluLeuAlaTyrAlaPheGlnThrGlyGlyValLeuTyrLeuIleGluGlyCysLeuSer 165
 DB 490 GATTATATTTATCCCTTTCAGACCGGTGAAACCTTACTCTCTCTGATATCTCAAT 549
 QY 166 GlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
 DB 550 GGAGGAGAACTATTTATGACATTAGAAAGAGGAGGATATTCATGAGAGATACAGCTTC 609
 QY 186 PheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIleIleTyr 205
 DB 610 TTTTACTGCTGAATATCTCAGCTGCTGGGCAATTCATCAAAAGGGGATATCTAC 669
 QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGlnGlyHisIleLeuLeuThrAsp 225
 DB 670 AGAGACTGAGACCGAGAAACATCATCTTAATCAACAAAGTCACTGAAAGCTGACAGAC 729
 QY 226 PheGlyLeuCysLeuSerIleHisGluGlyAlaValThrHisThrPheCysGlyThr 245
 DB 730 TTGGACTATGCAAAAGATCTATTCATGATGAAACGTCACGACCATTTTGTGAAACA 789
 QY 246 IleGlyTyrMetAlaProGluIleLeuValArgSerGlyHisAsnArgAlaValAspTyr 265
 DB 790 ATAGATATACATGGCCCTGAAATCTTGATGAGAGGCGCACACCGTCTGTGATGG 849
 QY 266 TrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGlu 285
 DB 850 TGGAGCTTGGAGCATTTAATGATGACATGCTGACGCGACCTCCATCTCGGGAG 909
 QY 286 AsnArgGlyLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProProTyrLeu 305
 DB 910 AATAGAAAGAGACATTTGACAAATCTCCAAATGAACTTAATTTGCTCTCACTC 969
 QY 306 ThrProAspAlaArgAspLeuValLysLysPheLeuLysArgAsnProSerGlnArgIle 325
 DB 970 AACAAGAGAGCTCGAATCTGCTTAAAGCTGCGAAGAAAGAAAGCTCTCGCTCT 1029
 QY 326 GlyGlyGlyProGlyAspAlaIleAspValGlnArgHisProPhePheArgHisMetAsn 345
 DB 1030 GGAAGCTGGCCCTGGGATGCTGAGAGAGTCCAGAGCCATCCATTTTTHAGACATTAAC 1089
 QY 346 TrpAspAspLeuLeuAlaTyrArgValAspProProPheArgProCysLeuGlnSerGlu 365
 DB 1090 TGGGAAGAGCTTTGGCTCGAAGGTGAGAGCCCTTTAAAGCTCTGTGCAATCTGAA 1149
 QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSerProAsp 385

DB 1150 GAGAGTGAAGTCAATTTGATTCAAAGTTACTGTCAGACCTCTTGAACAGCCCAT 1209
 QY 386 AspThrAlaLeuSerGlnSerAlaAsnGlnAlaPheLeuGlyPheThrTyrValAlaPro 405
 DB 1210 GACTCAACTCTCAGTGAAGATGCCAACAGAGGCTCTTGGGGTTTAAATATGCTGCA 1269
 QY 406 SerValLeuAspSerIleLysGluGlyLysPheSerPheGlnProCysLeuAspSerProGly 425
 DB 1270 TCTGTACTGAAGAGTGAAGAAAGATTTCTTTTGAACCAAAATCCGATCGCTGCA 1329
 QY 426 ArgLeuAsnSerSerProArgValProValSerProLeuLysPheSerProPheGlu--- 444
 DB 1330 AGATTATATGTGAGCCAGCAAGCCTGTGAGCCCAAGTCAATCTCTCTGGGAGATTC 1389
 QY 445 -----GlyPheArgProSerProSerLeuProGlu---ProThrGluLeuProLeu 460
 DB 1390 TGGGAGCAGAGGTGCTTCAAGCCAGCAGCAATCTCTGACACCTGTGAAATACCAATG 1449
 QY 461 ProProLeuLeuProProProProSerThrThr-----AlaProLeu 475
 DB 1450 GAAAGAGTGAATGACAGATGATGATGACCAAGAGCGGAGATTCAGCGGCACTT 1509
 QY 476 ProIleArgProPro---SerGlyThrLysLysSerLys 487
 DB 1510 CCAATCCGACAGCCCACTTGGGCTATACAAAAACAA 1548
 RESULT 8
 US-10-191-803-230
 / Sequence 230, Application US/10191803
 / Publication No. US20040014040A1
 / GENERAL INFORMATION:
 / APPLICANT: MENDRICK, Donna
 / APPLICANT: PORTER, Mark
 / APPLICANT: JOHNSON, Kory
 / APPLICANT: HIGGS, Brandon
 / APPLICANT: CASTLE, Arthur
 / APPLICANT: ELASHOFF, Michael
 / TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
 / FILE REFERENCE: 44921-5090US
 / CURRENT APPLICATION NUMBER: US/10/191, 803
 / PRIOR FILING DATE: 2002-07-10
 / PRIOR APPLICATION NUMBER: US 60/303, 819
 / PRIOR FILING DATE: 2001-07-10
 / PRIOR APPLICATION NUMBER: US 60/305, 623
 / PRIOR FILING DATE: 2001-07-17
 / PRIOR APPLICATION NUMBER: US 60/369, 351
 / PRIOR FILING DATE: 2002-04-03
 / PRIOR APPLICATION NUMBER: US 60/377, 611
 / PRIOR FILING DATE: 2002-05-06
 / NUMBER OF SEQ ID NOS: 1140
 / SOFTWARE: Patent Ver. 2.1
 / SEQ ID NO 230
 / LENGTH: 2287
 / TYPE: DNA
 / ORGANISM: Rattus norvegicus
 / FEATURES:
 / OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031985
 US-10-191-803-230
 Alignment Scores:
 Pred. No.: 6,54e-167 Length: 2287
 Score: 1740.00 Matches: 349
 Percent Similarity: 77.97% Conservative: 51
 Best Local Similarity: 68.03% Mismatches: 83
 Query Match: 66.56% Indels: 30
 DB: 16 Gaps: 8
 US-09-762-258-2 (1-495) x US-10-191-803-230 (1-2287)
 QY 1 MetAlaArgGlyArgArgAlaArgGlyAlaGlyAlaAla----- 13
 DB 22 ATGAGGAGAGACAGAGAGGCGGAGCGCTTTTACCCAGCGCTGACTTCCAGACAGGGA 81

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QY 14 -----MetAlaIaValPheAspLeuAspLeuGluThrGluGluGlySerGluGly 30
DB 82 GCTGAGGACATGCGAGAGTGTTCATGACCTGCGACCGACGAGAGTGCAGGCTCT 141
QY 31 GluGlyGluProGluLeuSerProAlaAspIaCysProLeuAlaGlu---LeuArgAla 49
DB 142 GAGCATGAGCTGAGAG-----GAGGGGGGTCTGATTAAATGAAAGCATGAGCAAT 189
QY 50 AlaGlyLeuGluPro-----ValGlyHisTyrGluGluValGluLeuThrGlu 65
DB 190 GGGGAGAGTTCAGCATGATGAACTTCGAAACATTCGTGAAATTCGAAATTCACAA 249
QY 66 ThrSerValAsnValGlyProGluArgGlyLeuGlyProHisCysPheGluLeuLeuArgVal 85
DB 250 ACTAGTGTGACAGAGGGCCGAGAAATTCAGACCAAGATGTTGACCTCTCTGGGCTA 309
QY 86 LeuGlyLysGlyGlyTyrGlyLysValPheGluValaGlyLysValGluGlyThrAsnLeu 105
DB 310 CTGGTAAAGGGGGCTATGAAAGGTTTTTCAAGTACGAAAGTAAAGGAGCAAGCAATCT 369
QY 106 GlyLysIleTyrAlaMetLysValLeuArgLysAlaLysIleValaArgAspAlaLysAsp 125
DB 370 GGAAGATATTTGGCATGATGAGTGTCTTAAAGGCAATGATGAGTAAAGTAAAGAT 429
QY 126 ThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValaLysHisProPheIleVala 145
DB 430 ACAGCTCATACAAAGCAAGGAGGAAATTCCTGAGAGAGTAAAGCATCCCTCATTTG 489
QY 146 GluLeuAlaIleTyrAlaPheGluThrGlyGlyLysLeuTyrLeuIleLeuGluCysLeuSer 165
DB 490 GATTATATTTATGCTTTCAGACCGTGGAAACCTTACCCATCCTTGAATCATCTAGT 549
QY 166 GlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeuGluAspThrAlaCys 185
DB 550 GAGAGGAGACTATTTATGCACTTGTAAAGAGAGGGGATATTCATGAGAGATACAGCTTC 609
QY 186 PheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGluGlyIleTyr 205
DB 610 TTTTATCTGGCTGAAATCTCATGCTTGGGCAATTCATCAAAAGGGGATATTCATC 669
QY 206 ArgAspLeuLysProGluAsnIleMetLeuSerSerGluGlyHisLeuLeuThrAsp 225
DB 670 AGAGACCTGAAAGCGGAGAACATGCTTAATATACCAAGGCTCAGGAACTGACAGAC 729
QY 226 PheGlyLeuCysLysGluSerIleHisGluGlyAlaValaThrHisThrPheCysGlyThr 245
DB 730 TTGGACTATGCAAGAGATCTATTCATGATGAGACAGTCAAGCACAATTTTGTGAGACA 789
QY 246 IleGlyTyrMetAlaProGluIleLeuValaArgSerGlyHisAspAlaValaAspTyr 265
DB 790 ATAGAATATGATGGCCCTGAAATCTTATGATGAAAGCGGCCCAACCGTGTGATGATGG 849
QY 266 TrpSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProProPheThrAlaGlu 285
DB 850 TGGAGCTCTGGAGACATTAATATGATGATGATGATGATGATGATGATGATGATGATG 909
QY 286 AsnArgLysLysThrMetAspLysIleIleArgGlyLysLeuAlaLeuProTyrLeu 305
DB 910 AATGAAAGAGAGCAATGATGCAAAATCTCTAAATGTAATTAATTCCTCCCTACCTC 969
QY 306 ThrProAspAlaArgAspLeuValaLysPheLeuLysArgAsnProSerGluArgIle 325
DB 970 ACACAAAGAGCTCGAGATCTGCTTAAAGCTGTGAAAGAAATGCTGCTTCCTGCTCT 1029
QY 326 GlyGlyGlyProGlyAspAlaAlaAspValaGlnArgHisProPhePheArgHisMetAsn 345
DB 1030 GAGAGCTGGCCCTGGGAGTGTGAGAGATGCCAAGCGCATCATTTTAAACACATTAAC 1089
QY 346 TrpAspAspLeuLeuAlaTyrArgValaAspProProPheArgProCysLeuGluSerGlu 365
DB 1090 TGGAGAGAGCTTTTGGCTCGAGAGTGGAGCGCCCTTAAAGCTCTGTTGCAATCTGAA 1149

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QY 366 GluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValaAspSerProAsp 385
DB 1150 GAGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1209
QY 386 AspThrAlaLeuSerSerGluSerAlaAsnGlnAlaPheLeuGluGlyPheThrTyrValaIlePro 405
DB 1210 GACTCAACTCTCATGATGAAAGTCCACACAGGCTCTTCTGGGTTTACATATGAGCTTCA 1269
QY 406 SerValaLeuAspSerIleLysGlyGlyPheSerPheGluProLysLeuArgSerProArg 425
DB 1270 TCTGATCTTGAAGATGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 1329
QY 426 ArgLeuAsnSerSerProArgValaProValaSerProLeuLysPheSerProPheGlu--- 444
DB 1330 AGATTATGTGTAGCCCAAGACCGCTGTGAGCCGACGCAAAATCTCTCTGGGAGATTTC 1389
QY 445 -----GlyPheArgProSerProSerLeuProGlu---ProThrGluLeuProLeu 460
DB 1390 TGGGAGAGAGTGTCTCAGGACAGCAGCAAAATCTCAGACACCTGTGAAATACCAATG 1449
QY 461 ProProLeuLeuProProProProProSerThrThr-----AlaProLeu 475
DB 1450 GAAACAGTGAATATGAGCAGATGATGATGATGATGATGATGATGATGATGATGATG 1509
QY 475 ProIleArgProPro---SerGlyThrLysLysSerLys 487
DB 1510 CCAATCCGACAGCCCAACTCTGGGCCCATACAAAGAAACAA 1548

```

RESULT 9

```

US-10-425-114-26874
: Sequence 26874, Application US/10425114
: Publication No. US20040034888A1
: GENERAL INFORMATION:
: APPLICANT: Liu, Jingdong
: APPLICANT: Zhou, Yihua
: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E.
: APPLICANT: Tabaska, Jack B.
: APPLICANT: Cao, Yongwei
: TITLE OR INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OR INVENTION: Plants and Uses Thereof for Plant Improvement
: FILER REFERENCE: 38-21(5313)B
: CURRENT APPLICATION NUMBER: US/10/425,114
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 26874
: LENGTH: 2362
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURES:
: OTHER INFORMATION: Clone ID: LIB4656-028-B10_FLI
US-10-425-114-26874

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Alignment Scores:

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Pred. No.: 2,59e-165 Length: 2362
Score: 1724.50 Matches: 351
Percent Similarity: 73.80% Conservative: 49
Best Local Similarity: 64.76% Mismatches: 79
Query Match: 65,974 Indels: 63
DB: 13 Gaps: 9

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US-09-762-258-2 (1-495) x US-10-425-114-26874 (1-2362)

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QY 1 MetAlaArgGlyArgArgAlaArgGlyAlaGlyAlaAla----- 13
DB 39 ATGAGGCGAGGAGAGGAGGCGGCTTTTACCCAGCCCGACTTCGAGACAGGAGAA 98
QY 14 -----MetAlaIaValPheAspLeuAspLeuGluThrGluGluGlySerGluGly 30
DB 99 GCTGAGGACATGCGAGATGTTTTCATGACATGACCTGAGACCAAGAGAGAGCGGGCTCT 158
QY 31 GluGlyGluProGluLeuSerProAlaAspAlaCysProLeuAlaGlu---LeuArgAla 49

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Db 159 GAGATGAGCTGGAG-----GAGGGGGGTGCTGTAATGAAGCATGACCAT 206
 Qy 50 AAGlyleuGluPro-----ValGlyHieTyrGluGluValGlyleuThrGlu 65
 Db 207 GGGGAGATGAGCTGACATGAGACTGGACATGGAATGGAATGGAATGGAATGGAAT 266
 Qy 66 ThrSerValasnaValGlyProGluArgGlyProHieCysPheGluLeuLeuArgVal 85
 Db 267 ACTAGTGTGAACAGAGGGCCAGAAAAATCAGACCGAAGATGTTTGAAGCTACCTCCGGTA 326
 Qy 86 LeuGlylyleuGlyGlyTyrGlylylValPheGlnValArglyValGlnGlyThrAsnLeu 105
 Db 327 CTGGTAAGGGGGCTATGAGAAAGGTTTCAAGTACGAAAGTAAACAGAGCAATACT 386
 Qy 106 GlylyleuValleuValleuValleuValleuValleuValleuValleuValleu 125
 Db 387 GGGAAATATTTGCTGATGAGAGTGTCTTAAAGGCAATGATGATGAAATGCTAAAGAT 446
 Qy 126 ThrAlaHieThrArgAlaGluArgAsnIleleuGluSerValIyshiSproPheIleVal 145
 Db 447 ACAAGCTCATCAAAAGAGAGAACGAAATATCTGAGAGAAATTAAGCATCCCTTCATCGTG 506
 Qy 146 GluLeuAlaTyrAlaPheGluThrGlyGlylylValleuThrleuGluCysleuSer 165
 Db 507 GATTATATTATGCTTCAAGCTGAGGAAAGCTTCACTGCTGAGATCTCACT 566
 Qy 166 GlylyleuLeuPheThrHieleuGluArgGlylylIlePheleuGluAspThrAla--- 184
 Db 567 GAGAGAGAACTATTATGCAAGTTAGAAAGAGAGAAATTTATGAGAGACACTGCTG 626
 Qy 184 ----- 184
 Db 627 CTGAGTGAACGCTCTTCAACACAGTGTCTTCAACAGAACCATTCATCGCGCTT 686
 Qy 185 -----CysPheTyrleuAlaGluIleThrleuAlaleuGlyHieAsnIser 200
 Db 687 CTTCCTGATGATGCTTTACTTGGAGAAATCTCATGCTTGGGCAATTTACATCA 746
 Qy 201 GlnGlyIleIleTyrArgAspleuLysProGluAsnIleleuLeuSerGlnGlyHie 220
 Db 747 AAGGGATCATCTACAGAGAGCTGAAAGCCGAGAAATATCATGCTATATACCAAGTCA 806
 Qy 221 IleIleLeuThrAspPheGlyleuCysIyGluSerIleHieGluGlyAlaValThrHie 240
 Db 807 GTGAACCTAACAGACTTGGACTATGCAAGAAATCTTTCATGATGAGAACAGTCAACAC 866
 Qy 241 ThrPheCysGlyThrIleGluTyrMetAlaProGluIleleuValArgSerGlyHieAsn 260
 Db 867 ACATTTGTGGAACATAGATATCATGSCCCCTGAATCTTGATGAGAGTGGCCACAT 926
 Qy 261 ArgAlaValAspThrPheSerleuGlyAlaIleuThrAspMetleuThrGlySerPro 280
 Db 927 CGTGTGTGATTTGGAGTTGGAGAGCTTATATATGACATGCTGAGAGACCC 986
 Qy 281 ProPheThrAlaGluAsnArglylylSerMetAspIyIleIleArglylylSerleuAla 300
 Db 987 CCATTCATCGGAGATGAGAAAGAAACATATGACAAATCTCAAAAGTAAACTCAT 1046
 Qy 301 LeuProProTyrleuThrProAspAlaArgAspleuValIylylPheleuLysArgAsn 320
 Db 1047 TTGCTCTCCCTACCTCAACAGAGAGCTGCTTAAAGAGCTGCTGAAAGAAAT 1106
 Qy 321 ProSerGlnArgIleGlylylGlyProGlyAspAlaAlaAspValGlnArgHieProPhe 340
 Db 1107 GCTGCTCTCTGCTGAGAGCTGCTCTGGGAGAGCTGAGAGAGTTCACATCATCATTC 1166
 Qy 341 PheArgHieMetAsnTyrAspAspleuLeuAlaTyrArgValAspProThrArgPro 360
 Db 1167 TTAGACATCTTACTAGGAGAAAGCTTCTGCTGAGAGAGTGGAGAGCTTAAACCT 1226
 Qy 361 CysleuGlnSerGluGluAspValIserGlnPheAspThrArgPheThrArgGlnThrPro 380
 Db 1227 CTTGTCATCTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1286

Qy 381 ValAspSerProAspAspThrAlaIleuSerGluSerAlaAsnGlnAlaPheleuGlyPhe 400
 Db 1287 GTGACAGCCCGAGAGACTCACTCATGATGAGAAATGCAATCAAGTCTTCTGGGTTT 1346
 Qy 401 ThrTyrValAlaProSerValleuAspSerIleIyGlyIyPheSerPheGlnProLys 420
 Db 1347 ACATATGTGCTCCCATCTGTACTTGAAGTGAAGAAAGATTTCCTTGAACCAAA 1406
 Qy 421 LeuArgSerProArgArgleuAsnSerSerProArgValProValIserProleuLysPhe 440
 Db 1407 ATCCCATACCTCGAAGATTTATTTGAGCCCAACACCACTGTGAGCCCAATTT 1466
 Qy 441 SerPro-----PheGluGlyPheArgProSerProSerleuProGluProThrGluLeu 458
 Db 1467 TCTCTGGAGATTTCTGGGAAAGAGCTCTTGGCCAC-----ACACCAAT 1514
 Qy 459 ProleuProProleuProProProProProSer----- 470
 Db 1515 CCTCAGACACTGTGGAATATCCCATATGAAAAGAGTGCATAGAGAGATGATGTGACA 1574
 Qy 471 -----ThrThrAlaProleuProIleArgProPro-----SerGlyThrIylyl 485
 Db 1575 ATGAGTGGGAGAGCATGCGCACACTTCAATACACAGCCGAATCTTGGGCAATACAA 1634
 Qy 486 SerIyys 487
 Db 1635 AAACAA 1640

RESULT 10
 US-09-925-298-245
 / Sequence 245, Application US/09925298
 / Publication No. US20020039764A1
 / GENERAL INFORMATION:
 / APPLICANT: Rosen et al.
 / TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 / FILE REFERENCE: PA103
 / CURRENT APPLICATION NUMBER: US/09/925,298
 / PRIOR FILING DATE: 2001-08-10
 / PRIOR APPLICATION NUMBER: PCT/US00/05861
 / PRIOR FILING DATE: 2000-03-08
 / PRIOR APPLICATION NUMBER: 60/124,270
 / NUMBER OF SEQ ID NOS: 845
 / SOFTWARE: ParentIn Ver. 2.0
 / SEQ ID NO 245
 / LENGTH: 1197
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / LOCATION: (218)
 / OTHER INFORMATION: n equals a,t,g, or c
 / NAME/KEY: misc feature
 / LOCATION: (1197)
 / OTHER INFORMATION: n equals a,t,g, or c
 / US-09-925-298-245

Alignment Scores:
 Pred. No.: 1,01e-157 Length: 1197
 Score: 1646.00 Matches: 309
 Percent Similarity: 98.72% Conservative: 0
 Best Local Similarity: 98.72% Mismatches: 3
 Query Match: 62.97% Indels: 1
 Gaps: 0

US-09-762-258-2 (1-495) x US-09-925-298-245 (1-1197)

Qy 184 AlaCysPheTyrleuAlaGluIleThrleuAlaleuGlyHieAsnIserGlnGlyIle 203
 Db 13 GCTGCTCTTCACTGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 72
 Qy 204 IleTyrArgAspleuLysProGluAsnIleleuSerGlnGlyHieIleTyrleu 223

Db 73 ATCAACGGAGACCTCAAGCCGAGAAACATCATGCTCAGACACCGGGCCATCAAACTG 132
Qy 224 ThrAspPheGlyLeuCyLeuGlySerIleHisGlyAlaValThrHisPheCys 243
Db 133 ACCGACTTTRACCTCTGCAAGAGCTATTCATGAGGGCCGCTCCTCATCACTTCTGCG 192
Qy 244 GlyThrIleGlyTyrMetAlaPro-GluIleLeuValArgSerGlyHisAsnArgAlaVal 263
Db 193 GGCACCATTTAGTACATGGCCCTGAGACATTTCTGGTGGCGAGTGGCCACAAACCGGGCTGT 252
Qy 263 LAspTyrPheSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPhePhe 283
Db 253 GGACTGGGAGGAGCTCGGGGGCCCTGATATACCACTGCTCCTGATGCGCCCTTTAC 312
Qy 283 -AlaGluAsnArgIleGlySerThrMetAspLeuIleIleArgIleGlyLeuLeuAlaLeuPro 303
Db 313 CGCAGAGAACCGGAGAAACCATGATGATCATCGGGGCAAGCTGGCACTGCCGCC 372
Qy 303 oTyrLeuThrProAspAlaArgAspLeuValIleValysPheLeuHisArgAsnProSerG 323
Db 373 CTACCTCAACCCCAAGATGCGGGAGCTGTCAAAAGTTCTGAAACGGAAATCCACGCA 432
Qy 323 nArgIleGlyGlyIleProGlyAspAlaAlaAspValGlnArgHisProPhePheArgH 343
Db 433 GCGGATTGGGGGTGGCCCAAGGGAGATGCTGATGTGCAAGACATCCCTTTTCCGGCA 492
Qy 343 sMetAsnTyrAspAspLeuLeuAlaTyrArgValAspProProPheArgProCysLeuG 363
Db 493 CATAAATTTGGACACCTCTTGGGCTGCGCTGGTGGAGACCCCTTTCAGGGCCCTGTGCA 552
Qy 363 nSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSe 383
Db 553 GTGAGAGAGAGACGTGAGCCAGTTGATACCCGCTTCAACGGCAGACGCGGTGGACAG 612
Qy 383 rProAspAspThrAlaLeuSerGlySerAlaAsnGlnAlaPheLeuGlyPheThrTyrVa 403
Db 613 TCCTGATGACACAGCCCTCAGCGAGACTGCCAACAGGCTTCTCGGGCTTCAATACGT 672
Qy 403 lAlaProSerValLeuAsnSerIleIleGlyGlyPheSerPheGlnProIleLeuArgSe 423
Db 673 GAGCCCTCTGTCTGAGACACATCAAGAGGCTTCTTCCAGCCCAAGCTTGGCTC 732
Qy 423 rProArgArgLeuAsnSerSerProArgValProValSerProLeuHisPheSerPro 443
Db 733 ACCAGGCGCCTCAACAGTAGACCCCGGGGCCCGCTCAGCCCTCAAGTTCTCCCTTT 792
Qy 443 eGluGlyPheArgProSerProSerLeuProGluProThrGluLeuProIleProIle 463
Db 793 TGAAGGGATTGCGCCAGCCCAAGCTGCGAGAGCCACAGAGCTTACCTTACCTCACT 852
Qy 463 uLeuProProProProSerThrThrAlaProLeuProIleArgProProSerGlyTh 483
Db 853 CTGGCAGCGCGCGCGCCCTCGAGACACCGCCCTCTCCCATCGTCCCGCCCTCAAGGAC 912
Qy 483 rLysLysSerLysArgGlyArgGlyArgProGlyArg 495
Db 913 CAAGAACTCCAAAGAGGGCGCTGGCGCTTCAGAGGGCGC 949

RESULT 11

US-10-102-806-245
Sequence 245, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: P4103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 245
LENGTH: 1197
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (218)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1193)
OTHER INFORMATION: n equals a,t,g, or c
US-10-102-806-245
Alignment Scores:
Pred. No.: 1,01e-157 Length: 1197
Score: 1646.00 Matches: 309
Percent Similarity: 98.72% Conservative: 0
Best Local Similarity: 98.72% Mismatches: 3
Query Match: 62.97% Indels: 1
DB: 15 Gaps: 0
US-09-762-258-2 (1-495) x US-10-102-806-245 (1-1197)
Qy 184 AlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSerGlnGlyIle 203
Db 13 GCGTGTCTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 72
Qy 204 lIleTyrArgAspLeuAspProGluAsnIleMetLeuSerSerGlnGlyHisIleLysLeu 223
Db 73 ATTACCGGAGACCTCAAGCCCGAGAACATCACTCTCAGAGCCAGGGCCATCAAACTG 132
Qy 224 ThrAspPheGlyLeuCyLeuGlySerIleHisGlyAlaValThrHisPheCys 243
Db 133 ACCGACTTTRACCTCTGCAAGAGCTATTCATGAGGGCCGCTCCTCATCACTTCTGCG 192
Qy 244 GlyThrIleGlyTyrMetAlaPro-GluIleLeuValArgSerGlyHisAsnArgAlaVal 263
Db 193 GGCACCATTTAGTACATGGCCCTGAGACATTTCTGGTGGCGAGTGGCCACAAACCGGGCTGT 252
Qy 263 LAspTyrPheSerLeuGlyAlaLeuMetTyrAspMetLeuThrGlySerProPhePhe 283
Db 253 GGACTGGGAGGAGCTCGGGGGCCCTGATATACCACTGCTCCTGATGCGCCCTTTAC 312
Qy 283 -AlaGluAsnArgIleGlySerThrMetAspLeuIleIleArgIleGlyLeuLeuAlaLeuPro 303
Db 313 CGCAGAGAACCGGAGAAACCATGATGATCATCGGGGCAAGCTGGCACTGCCGCC 372
Qy 303 oTyrLeuThrProAspAlaArgAspLeuValIleValysPheLeuHisArgAsnProSerG 323
Db 373 CTACCTCAACCCCAAGATGCGGGAGCTGTCAAAAGTTCTGAAACGGAAATCCACGCA 432
Qy 323 nArgIleGlyGlyIleProGlyAspAlaAlaAspValGlnArgHisProPhePheArgH 343
Db 433 GCGGATTGGGGGTGGCCCAAGGGAGATGCTGATGTGCAAGACATCCCTTTTCCGGCA 492
Qy 343 sMetAsnTyrAspAspLeuLeuAlaTyrArgValAspProProPheArgProCysLeuG 363
Db 493 CATAAATTTGGACACCTCTTGGGCTGCGCTGGTGGAGACCCCTTTCAGGGCCCTGTGCA 552
Qy 363 nSerGluGluAspValSerGlnPheAspThrArgPheThrArgGlnThrProValAspSe 383
Db 553 GTGAGAGAGAGACGTGAGCCAGTTGATACCCGCTTCAACGGCAGACGCGGTGGACAG 612
Qy 383 rProAspAspThrAlaLeuSerGlySerAlaAsnGlnAlaPheLeuGlyPheThrTyrVa 403
Db 613 TCCTGATGACACAGCCCTCAGAGAGACTGCCAACAGGCTTCTCGGGCTTCACTACT 672
Qy 403 lAlaProSerValLeuAspSerIleIleGlyGlyPheSerPheGlnProIleLeuArgSe 423


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Db      673 GGGCGCGCTCTCTCGACAGCATCAAGAGGCGTCTCTCTCCAGCCAGCTGCGCTC 732
Qy      423 rProArgArgLeuAnsSerSerProArgValProValSerProLeuIysPheSerProPh 443
Db      733 ACCAGGCGCGCTCAACAGTAGAGCCCCCGGCGCCCGCTGAGCCCTCAAGTCTCCCTTT 792
Qy      443 eGluGlyPheArgProSerProSerLeuProGluProThiGluLeuProLeuProLe 463
Db      793 TGAAGGGCTTCGCGCCAGCCCGAGCTGCGCGAGCCACCGAGCTACCTTACCTCAGCT 852
Qy      463 uLeuProProProProProSerThiThiAlaProLeuProIleArgProProSerGlyTh 483
Db      853 CTTCGCCCGCGCGCGCGCTCGACCGCGCGCTCTCTCCAGTCCGTCGCCCTCGAGGAC 912
Qy      483 rLysLysSerLysArgLysArgLysArgLysArgLysArgLysArgLysArgLysArg 495
Db      913 CAAGAGTCCAGAGAGGCGCGCTGCGCGCTCCAGGCGCGC 949

RESULT 12
US-09-817-310-1
; Sequence 1, Application US/09817310
; Patent No. US20010042254A1
; GENERAL INFORMATION:
; APPLICANT: Kozma, Sarah
; APPLICANT: Stewart, Mary
; APPLICANT: Thomas, George
; TITLE OF INVENTION: Drosophila melanogaster P70 S6 Kinase
; FILE REFERENCE: 4-20971/A
; CURRENT APPLICATION NUMBER: US/09/817,310
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 09/230,247
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentr Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2556
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-817-310-1

Alignment Scores:
Pred. No.:      8,096-138      Length:      2556
Score:          1455.00      Matches:      309
Percent Similarity: 66.73%      Conservative: 52
Best Local Similarity: 57.12%      Mismatches: 115
Query Match:    55.66%      Indels:      65
DB:             9      Gaps:      10

US-09-762-258-2 (1-495) x US-09-817-310-1 (1-2556)
Qy      13 AlawerAlaAlaVal-----PheAspLeu-----AspLeuGlu 23
Db      471 GCATGGCGGACGTCGACCGATCCAGGAACTGTTCAGCTGAGCTGACGACGCGAA 530
Qy      24 ThrcGluGlySerGluGlyGlyGluPro-----GluLeuSerProAlaAsp 40
Db      531 CTGACAGACGACCAAGCGCAGGACTCCAGACGACGACGAGATCGAGCTGACGAGCTTAC 590
Qy      41 AlaCySerProLeuAlaGluLeuArgAlaAlaGlyLeuGluProValGlyHisTyrgLuglu 60
Db      591 CTAGAACCG-----GAATTGTGTATTAATCTGCACCAAGACACTGAGCGCGCAGAGACC 644
Qy      61 ValGluLeuThrgLugluThrservalAsnValGlyProGluArgGlyProHisCySerPhe 80
Db      645 ATACAGCTCTGCGAGGAAATGTATTCAGGTAAATCAAGCTGAGCGGACCCAGAACTTT 704
Qy      81 GluLeuLeuArgValLeuGlyLysGlyTyrgLysValPheGluValArgLysVal 100
Db      705 GAGCTCAAGAGAGCTCTTGCGAAGCGGTTATTCAGGATTTTCAGGTGCGCAGACC 764
Qy      101 GlnGlyThrsanLeuGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLys 120
Db      765 GCTGAGAGAGATGCTAACAAATATTTTGCATGAGAGGTGCTCAAAAAGGATCATATG 824

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Qy      121 ArgAsnAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeuGluSerValIys 140
Db      825 ACCAATCAAAAGAGACAGCGCACCGCGCGCAGCGCAATATCTCGAGGACGACAG 884
Qy      141 HisProPheIleValGluLeuAlaTyraAlaPheGlnThrgLysGlyLeuLeuTyrrLeuIle 160
Db      885 CATCCCTTCATAGTGAAGCTATGATTAAGCTTTCAGACGACGAGAAACTATACCTTAA 944
Qy      161 LeuGluCyLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGluGlyIlePheLeu 180
Db      945 CTGAAATATCTCAGCGGCTGAGAGCTGTTCAAGCATTTTGACGTCGAGGAGCATCTTCTA 1004
Qy      181 GluAspThrAlaCyPheTyrrLeuAlaGluIleThrLeuAlaLeuGlyHisLeuHisSer 200
Db      1005 GAGGATACCAACATGCTTCTATCTTAAGCAAAATATTTGGCTTGGCCATCTTACACAA 1064
Qy      201 GlnGlyIleLeuTyraArgAspLeuLysProGluAsnIleMetLeuSerSerGlnIyHis 220
Db      1065 CTGGGATCATCTTACCGCATCTGAAAGCCGAGAAACATCTGCTCGATGACAGAGGACAT 1124
Qy      221 rLysLysLeuThrsPheGlyLeuCyLysGluSerIleHisGluGlyAlaValThrsHis 240
Db      1125 GTGAAGCTCAGGAGCTTGTGACTGTGCAAGAGACATACAGAGGATATTGTCAACCCAC 1184
Qy      241 ThrPheCyGlyThrIleGluTyrrMetAlaProGluIleLeuValArgSerGlyHisAsn 260
Db      1185 ACCCTCTGCGGACCAATTAAGTAATGACCTGAAATTTTACCAAGAGTGGCCATGCG 1244
Qy      261 ArgAlaValAspTrpTrpSerLeuGlyAlaLeuMetTyraPheMetLeuThrgLysPro 280
Db      1245 AAAGAGTGAAGTGGTGTGACTGGCGGCTCTCATGTTGACATGCTCACAGAGTCCCA 1304
Qy      281 ProPheThrAlaGluAsnArgLysLysThrsMetAspLysIleIleArgGlyLysLeuAla 300
Db      1305 CCCTTCACCGCGAAGATGCAAGAGACCATGACCAATCTGAAACCCAGGCTCAAT 1364
Qy      301 LeuProTyrrLeuThrsProAspAlaArgAspLeuValLysLysPheLeuLysArgAsn 320
Db      1365 CTGCCAGCTTACTACACCGGAGACCGAGATCTGTGCTGCTGCTGATGAAGCGGACAG 1424
Qy      321 ProSerGluArgIleGlyGlyGlyProGlyAspAlaAlaAspValGluArgHisProPhe 340
Db      1425 GAACCTCAGCGGCTTGGACCGGACCGGACGAGATGCGCGCTGTTCAAAATACACCATTC 1484
Qy      341 PheArgHisMetAsnTrpAspAspLeuLeuAlaTrpArgValAspProProPheArgPro 360
Db      1485 TTCAAAACAGTCAACTGGGACATGTGCTCGCCAGACGCTGAGCGCGCTTAATAACCG 1544
Qy      361 CysLeuGlnSerGluGluAspValSerGluPheAspThrArgPheThrArgGlnThrsPro 380
Db      1545 CTCTTGAGAGAGCGAGATATGCTCACAGTTCGATACAGATTCCAGAGAACAAATCCCA 1604
Qy      381 ValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGluAlaPheLeuGlyPhe 400
Db      1605 GGGATTCCTCGATGATACAGCTTACAGCTTACAGGAAAGTCCAAATTTATTTCCAGTTTC 1664
Qy      401 ThrTyraAlaProSerValLeuAspSerIleLysGluGlyPheSerPheGlnProLys 420
Db      1665 ACTTACGTTGACACCTCGATCTGAGGATATGATCGG-----GCCAACCGAGATGCCA 1718
Qy      421 LeuArgSerProArgArgLeuAsnSerSerProArgValProValSer----- 436
Db      1719 GCAAGCTCCCGACAGAGCATCGACGACGCTGCCGAGACAGAGCTTCGCGCTGCGAGTTTC 1778
Qy      437 -----ProLeuLysPheSerProPheGluGlyPhe----- 446
Db      1779 CCATGCGCAATGTGGCGCGCATGTGCTGCGCATGACGCGCATTCGCGAGGATC 1838
Qy      447 -----ArgProSe 449
Db      1839 CGGAGTGTTCAGACAGACCGCGCGCGATCATGACATGACATTTGGCGCGCGTTCATTC 1898

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Alignment Scores:

Pred. No.:	5,13e-131	Length:	1607
Score:	1385.50	Matches:	285
Percent Similarity:	70.65%	Conservative:	40
Best Local Similarity:	61.96%	Mismatches:	69
Query Match:	53.00%	Indels:	67
	16	Gaps:	10

US-09-762-258-2 (1-495) x US-10-305-720-126 (1-1607)

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Qy      86 LeuGlyysgLygLygLygValPheGlnValArgLysValGlnGlyThrAsnLeu 105
Db      227 CTGGGGAGGCGCTCATGCCAGTGCAGACTGC-----ATTACCTG 271
Qy      106 -----GlyLysIleTyraLysMetLysValLeuArg-----LysAla 117
Db      272 ATCACCGACGAGAGTACCCGCTCAATATCATGTTTTTTTCAGGCGCACATTCCGAGC 331
Qy      118 LysIleValArgAlaLysAspThrAlaHisThrArgAlaGluArgAlaLysLeu 137
Db      332 AGGGTTTCAGGAGGTGAGATGCTGTACCGAGTCCAGGAGACAGAAAGCTCTAGAG 391
Qy      138 SerValLysHisProPheIleValGluLeuAlaTyraLysPheGlnThrGlyLysLeu 157
Db      392 CTGATTGAGTTC-----TTCCAGAGAGAGAGCCGCTTC 424
Qy      158 TyrlleuIleuGlyCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGly 177
Db      425 TACCGGTGTTTGAAGATGCGGGAGAGCTCCATCTCGACCAATCCACAAAGCCGCG 484
Qy      178 IlePheLeuGluAspThrAlaCysPheTyrlleuAlaGluIleThrLeuAlaLeuGlyHis 197
Db      485 CACTTCACAGAGCTGAGAGCCAGCGTGTGTGTGAGAGACCTGCCAGCGCTTGAGACTT 544
Qy      198 LeuHisSerGlnGlyIleIleTyraArgAspLeuLysProGluAsnIleMetLeuSerSer 217
Db      545 CTCGATTAACAAGGATGCGCCCAAGAGGACCTTAAGCCGGAACATCTCTGTGAGAC 604
Qy      218 GlnGlyHis-----IleLysLeuThrAspPheGlyLeu----- 228
Db      605 CCCAACAGGCTCTCCCGGAGATGTGACCTTGACCTCGAGCGAGCGGCATCAAACTC 664
Qy      229 -----CysLysGlnSerIleHisGlyIleAla-ValThrHisThrPheCysGly 245
Db      665 AACGGGAGCTGCTCCCTAT-CTCCACCCCGAGAGCTCTCAGCTCG-----TGGCGCTC 717
Qy      245 rIleGluTyrMetAlaProGluLe----- 253
Db      718 GCGGAGATACATGCGCCCGAGAGTGTGAGAGCTTCAGCGAGAGCTACATTCAG 777
Qy      254 -----LeuValArgSerGlyHisAs 260
Db      778 CAAGCGCTGACCTGTGAGAGCTGCGGCTCATCTTATATCTATCTACTGACGCGGATCC 837
Qy      260 naGAlaValAsp---TrpTrpSer-----LeuGlyAlaLeuMetTyrAspMetLe 276
Db      838 GCCCTTGCTGAGCGCTGTGTGAGAGCGACTGCGGCTGAGAGCCGCTATGTACACATGCT 897
Qy      276 uThrGlySerProPheThrAlaGluAsnArgLysLysThrMetAspLysIleLeu 296
Db      898 CACTGATCGCGCTTTCACCGAGAGAACCGGAAGAAACATGATAGATCATCCAG 957
Qy      296 gGlyLysLeuAlaLeuProProTyrLeuThrProAspAlaArgAspLeuValLysPhe 316
Db      958 GGGCAAGCTGCACTTCCCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 1017
Qy      316 eleuLysArgAspProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValG 336
Db      1018 TCTGAATCGAATCTCCAGCGAGATGGGGGTGGCGCGGAGATCTCTCTATATGCA 1077
Qy      336 naGHisProPheThrArgHisMetAsnTyrAspAspLeuLeuAlaTyrArgValAspPr 356
Db      1078 GAGAGATCCCTTTTTCGGGACATGATTTGGAGAGACCTTCTGCGCTGCGGTGTGAGACC 1137

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Qy      356 oProPheArgProCysLeuGlnSerGluGluAspValSerGlnPheAspThrArgPhe 376
Db      1138 CCGTTTCAGGCGCTGTCTGTCACTGACAGAGAGACGAGACCACTTTGATACCCGCTTAC 1197
Qy      376 rArgGlnThrProValAspSerProAspAspThrAlaLeuSerGlnSerAlaAsnGlnAl 396
Db      1198 ACGGCAAGAGCGCGGTGACATGCTGATGACACAGCCCTCAGAGAGTGCACACAGAGC 1257
Qy      396 aPheLeuGlyPheThrTyrValAlaProSerValLeuAspSerIleLysGlyGlyPhe 416
Db      1258 CTTCCTGAGCTTCACTACCTGAGCGCGCTGTCTGTCTGTGACAGATCAAGAGAGCTTTC 1317
Qy      416 rPheGlnProLysLeuArgSerProArgArgLeuAsnSerSerProArgValProVal 436
Db      1318 CTTCAGAGCCAGAGCTGCGCTCAACAGAGCGCTCAACATGATACCCCGGCTCCGCTCAG 1377
Qy      436 rProLeuLysPheSerProPheGluGlyPheArgProSerProSerLeuProGluProth 456
Db      1378 CCGCTCAAGTCTCTCCCTTTGAGGGGTTTGAGCCCAAGCCCAAGCTTCGAGAGCCAC 1437
Qy      456 rGluLeuProLeuProProLeuLeuProProProProSerThrAlaProLeuPr 476
Db      1438 GGAGCTACCTTACCTCCACTCTGCAACGCGCGCGCGCTGACCAACCGCCCTCTCC 1497
Qy      476 oIleArgProProSerGlyThrLysSerLysArgGlyArgGlyArgProGlyArg 495
Db      1498 CATTGCTCCCTCCCTCAAGGACCAAGAGTCCAAAGAGGGGCGGTGAGGCGGTCAAGGGCGT 1555

RESULT 15
US-10-220-955-1
; Sequence 1: Application US/10220955
; Publication No. US20030211989A1
; GENERAL INFORMATION:
; APPLICANT: PLOMMAN, GREGORY D.
; APPLICANT: WHITE, DAVID
; APPLICANT: MANNING, GERARD
; APPLICANT: SUDARSANAM, SUCHA
; APPLICANT: MARTINEZ, RICARDO
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES AND PROTEIN KINASE-LIKE
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: 038602-1401
; CURRENT APPLICATION NUMBER: US/10/220,955
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-220-955-1

Alignment Scores:
Pred. No.: 1,12e-113
Score: 1211.50
Percent Similarity: 90.07%
Best Local Similarity: 79.43%
Query Match: 46.35%
DB: 13
Gaps: 1

US-09-762-258-2 (1-495) x US-10-220-955-1 (1-843)
Qy      117 AlaLysIleValArgAspAlaLysAspThrAlaHisThrArgAlaGluArgAsnIleLeu 136
Db      1 GGAATGATGATGAGAAATGCTAAAGATACGCTCATTAACAAAGAGAGATGAAATTTCTG 60
Qy      137 GluSerValLysHisProPheIleValGluLeuAlaTyraLysPheGlnThrGlyLys 156
Db      61 GAGGAAGTAGGACATCCCTTATGATTTAATTAATGCTTCAAGCTGCTGAGAAAA 120
Qy      157 LeuTyrLeuIleuGlyCysLeuSerGlyGlyGluLeuPheThrHisLeuGluArgGly 176
Db      121 CTCTACTCATCTCTTGAAGATCTCAGTGAAGAGAACTATTATTACGATTAAGAAAGAG 180

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QY 177 GlyIlePheLeuGluAspThrAlaCysPheTyrLeuAlaGluIleThrLeuAlaLeuGly 196
DB 181 GGAATATTATTATGAGAGACCTGCTGCTTTACTTGGCAGAAATCTCCATGCGCTTGGGA 240
QY 197 HistLeuHisSerGlnGlyIleIleTyrArgAspLeuLysProGluAsnIleMetLeuSer 216
DB 241 CATTACATCAAAAGGGGATCATATACAGAGACTGGAAGCCGAGAGAAATATCATTTTAAAT 300
QY 217 SerGlnGlyHisIleLeuLeuThrAspPheGlyLeuCysLysGluSerIleHisGluGly 236
DB 301 CACCAAGGTCATATGAAAGCTAACAAGACTTGGACTAAGGAAAGATCATATCATATGGA 360
QY 237 AlaValThrHisThrPheCysGlyThrIleGluTyrMetAlaProGluIleLeuValArg 256
DB 361 ACAGTCACACACACATTTTGTGGACAAATAGATATCATGCCCCCTGAAATCTTGATGAGA 420
QY 257 SerGlyHisAsnArgAlaValAspThrPheSerLeuGluAlaLeuMetTyrAspMetLeu 276
DB 421 AATGACCAATCGATGCTGTGGATGGAGATTGGAGCATATATGATGACATGCTG 480
QY 277 ThrGlySerProProPheThrAlaGluAsnArgLysLysThrMetAspLysIleIleArg 296
DB 481 ACTGAGACACCCCCATTTACTGGGAGATAGAGAAAGAAACAATGACACATCCTCAA 540
QY 297 GlyLysLeuAlaLeuProProTyrIleuThrProAspAlaArgAspLeuValLysPhe 316
DB 541 TGTAACTCAATTGTGCTCTTACTCTCACACAAAGCCAGAGATCTGTTAAAAAGCTG 600
QY 317 LeuLysArgAsnProSerGlnArgIleGlyGlyProGlyAspAlaAlaAspValGln 336
DB 601 CTGAAAGAAAGATGCTTCTCT--CTGGAGCTGTCTCTGGGACGCTGAGAAATTCA 657
QY 337 ArgHisProPhePheArgHisMetCAsnTrpAspAspLeuAlaTrpArgValAspPro 356
DB 658 GCTCATTCATCTTTAGACACATTAAGTGGAGAACTTCTGGCTCAAAAGGTGAGGCC 717
QY 357 ProPheArgProCysLeuGlnSerGlnGluAspValSerGlnPheAspThrArgPheThr 376
DB 718 CTTTTTAAACCTCTGTGCAATCTGAAAGAGATGTAAGTCAAGTTGATTCAGATTACA 777
QY 377 ArgGlnThrProValAspSerProAspAspThrAlaLeuSerGluSerAlaAsnGlnAla 396
DB 778 CGTGAGACACCTGTGACAGCCAGATGACGCACTCATGGAATGCAATCAGGTC 837
QY 397 PheLeu 398
DB 838 TTCTG 843
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Search completed: July 3, 2004, 13:52:59
Job time : 711 secs

QY 206 CTGCGAGTTGAGGCGAGCTGCGCTAGAGCTGTGGAACAATGAGAGGTGAGCTG 265
 DB 152 CTGCGAGTTGAGGCGAGCTGCGCTAGAGCTGTGGAACAATGAGAGGTGAGCTG 211
 QY 266 ACTGAGACCAAGCTGTAAGCTTGGCCGAGAGCGATGGGCGCCCACTGCTTTGAGCTG 325
 DB 212 ACTGAGACCAAGCTGTAAGCTTGGCCGAGAGCGATGGGCGCCCACTGCTTTGAGCTG 271
 QY 326 CGTGTGCTGGGCAAGGGGGGCTATGGAAGTGTTCAGAGTGGAAAGGTGCAAGGCGC 385
 DB 272 CGTGTGCTGGGCAAGGGGGGCTATGGAAGTGTTCAGAGTGGAAAGGTGCAAGGCGC 331
 QY 386 AACTGGGCAAAATATATGCAATGAAAGTCTTAAGAGGCGCAAAATGTCGCAATGCGC 445
 DB 332 AACTGGGCAAAATATATGCAATGAAAGTCTTAAGAGGCGCAAAATGTCGCAATGCGC 391
 QY 446 AAGGACACAGCAACAACGAGGCTGAGCGGGAACATCTAGAGTCAATGAAAGCGCCCTTT 505
 DB 392 AAGGACACAGCAACAACGAGGCTGAGCGGGAACATCTAGAGTCAATGAAAGCGCCCTTT 451
 QY 506 ATTGTGGAATGAGCTATGCTTCAAGCTGTGGAACCTTACCTCACTCTTGAAGTGC 565
 DB 452 ATTGTGGAATGAGCTATGCTTCAAGCTGTGGAACCTTACCTCACTCTTGAAGTGC 511
 QY 566 CTGAGTGTGGCGAGCTTCAAGCACTGTGAGAGGAGGCACTTCTGGAAGTGC 625
 DB 512 CTGAGTGTGGCGAGCTTCAAGCACTGTGAGAGGAGGCACTTCTGGAAGTGC 571
 QY 626 GCTGTCTTACTGCTGCTGAGATCAGCTGCGCCCTGGGCACTTCCAGCGGCGATC 685
 DB 572 GCTGTCTTACTGCTGCTGAGATCAGCTGCGCCCTGGGCACTTCCAGCGGCGATC 631
 QY 686 ATCTACCGGAGCCTCAAGCCCGAGAAATCATCTCAGAGCGGCGCAATCAAACTGC 745
 DB 632 ATCTACCGGAGCCTCAAGCCCGAGAAATCATCTCAGAGCGGCGCAATCAAACTGC 691
 QY 746 ACCGACTTTGAGCTGCAAGAGGATCATCTCAGAGCGGCGCTGCTCACTCACTCTTGC 805
 DB 692 ACCGACTTTGAGCTGCAAGAGGATCATCTCAGAGCGGCGCTGCTCACTCACTCTTGC 751
 QY 806 GAGCACTTGAATGATGAGCGCCCTGAGATTTCTGTGCGGAGTGGCCACAACCGGCGTGC 865
 DB 752 GAGCACTTGAATGATGAGCGCCCTGAGATTTCTGTGCGGAGTGGCCACAACCGGCGTGC 811
 QY 866 GACTGTGAGAGCTGCGGGGCGCTGAGTACGAGATCTCACTGAGATGCGCGCTTAC 925
 DB 812 GACTGTGAGAGCTGCGGGGCGCTGAGTACGAGATCTCACTGAGATGCGCGCTTAC 871
 QY 926 GCAAGAACCGGAGAAACCATGATTAAGATCATGAGGCGCAAGCTGCACTGCGCCGC 985
 DB 872 GCAAGAACCGGAGAAACCATGATTAAGATCATGAGGCGCAAGCTGCACTGCGCCGC 931
 QY 986 TACCTCAACCCAGATCCCGGAGCTTGTCAAAATTTCTGAAACGGAATCCGAGCGAG 1045
 DB 932 TACCTCAACCCAGATCCCGGAGCTTGTCAAAATTTCTGAAACGGAATCCGAGCGAG 991
 QY 1046 CGGATTGGGGTGGCCCAAGGAGTGTGCTGATGTGCAAGACATCCCTTTTCCGGCAC 1105
 DB 992 CGGATTGGGGTGGCCCAAGGAGTGTGCTGATGTGCAAGACATCCCTTTTCCGGCAC 1051
 QY 1106 ATGAAATTTGGAACCACTTGTGCGCTGGCGGTGGAAGGCGCCCTTTCAGGCGCTGTGAG 1165
 DB 1052 ATGAAATTTGGAACCACTTGTGCGCTGGCGGTGGAAGGCGCCCTTTCAGGCGCTGTGAG 1111
 QY 1166 TCAGAGAGAGCTGAGCAAGTTGATACCCGCTTTCACAACGAGCAAGCGCGGTGAGCACT 1225
 DB 1112 TCAGAGAGAGCTGAGCAAGTTGATACCCGCTTTCACAACGAGCAAGCGCGGTGAGCACT 1171
 QY 1226 CCGTAAGTACCAAGGCTTGAAGGAGTGTGCAACCAAGGCGCTTCTGCGCTTTCACATACG 1285
 DB 1172 CCGTAAGTACCAAGGCTTGAAGGAGTGTGCAACCAAGGCGCTTCTGCGCTTTCACATACG 1231
 QY 1286 GCGCGCTTGTCTGTGAGCAAGATCAAGAGGCGCTTCTTCCAGGCGCAAGGCTGCGCTCA 1345

DB 1232 GCGCGCTGTGTCTGTGAGAGGATCAAGAGGCGCTTCTCTTCCAGCCCAAGCTGCGCTCA 1291
 QY 1346 CCGAGGCGCTTCAACAGTATAGCCCCCGGATCCCGGTCAAGCCCTCAAGTTCTCCCTTTT 1405
 DB 1292 CCGAGGCGCTTCAACAGTATAGCCCCCGGATCCCGGTCAAGCCCTCAAGTTCTCCCTTTT 1351
 QY 1406 GAGGCGTTTCCGCGCCAGCCCAAGCTGCGGAGCCCAAGAGCTACCTTCACTTCACTC 1465
 DB 1352 GAGGCGTTTCCGCGCCAGCCCAAGCTGCGGAGCCCAAGAGCTACCTTCACTTCACTC 1411
 QY 1466 CTGCAACCGCGCGCCCTTCAAGCAAGCCCTCTTCCCATCTCCGTCCCGCTCAAGAGCC 1525
 DB 1412 CTGCAACCGCGCGCCCTTCAAGCAAGCCCTCTTCCCATCTCCGTCCCGCTCAAGAGCC 1471
 QY 1526 AAGAGTCTCAAGAGGCGCGTGGGCGTCCAGGCGCTGAGGAGCGGAGTGGGAGTGAAGG 1585
 DB 1472 AAGAGTCTCAAGAGGCGCGTGGGCGTCCAGGCGCTGAGGAGCGGAGTGGGAGTGAAGG 1531
 QY 1586 TAGCCCTTGAAGCCCTGTCTGCGGCTGTGAGAGCAAGAGACCTTGGGCGCAATTCCAGA 1645
 DB 1532 TAGCCCTTGAAGCCCTGTCTGCGGCTGTGAGAGCAAGAGACCTTGGGCGCAATTCCAGA 1591
 QY 1646 GACCTGGGAGTGTGTCTGGGAGTGGGAGTGTGAGTGCATGAAAGTGTGTCTGCTGAG 1705
 DB 1592 GACCTGGGAGTGTGTCTGGGAGTGGGAGTGTGAGTGCATGAAAGTGTGTCTGCTGAG 1651
 QY 1706 GCAAGCTGAGCCCTTGAATCATGAGCAAGAGGCGCGCCGCAACCCCGGCTCAACTG 1765
 DB 1652 GCAAGCTGAGCCCTTGAATCATGAGCAAGAGGCGCGCCGCAACCCCGGCTCAACTG 1711
 QY 1766 CTCCCGTGAAGATTAAGGCGCTGAATCATG 1796
 DB 1712 CTCCCGTGAAGATTAAGGCGCTGAATCATG 1742

RESULT 2
 US-09-925-298-245
 / Sequence 245: Application US/09925298
 / Publication No. US20020039764A1
 / GENERAL INFORMATION:
 / APPLICANT: Rosen et al.
 / TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 / FILE REFERENCE: PA103
 / CURRENT APPLICATION NUMBER: US/09/925,298
 / PRIOR FILING DATE: 2001-08-10
 / PRIOR APPLICATION NUMBER: PCT/US00/05881
 / PRIOR FILING DATE: 2000-03-08
 / PRIOR APPLICATION NUMBER: 60/124,270
 / NUMBER OF SEQ ID NOS: 846
 / SOFTWARE: PatentIn Ver. 2.0
 / SEQ ID NO 245
 / LENGTH: 1197
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / FEATURE:
 / NAME/KEY: misc feature
 / LOCATION: (218)
 / OTHER INFORMATION: n equals a,t,c,g, or c
 / NAME/KEY: misc feature
 / LOCATION: (1193)
 / OTHER INFORMATION: n equals a,t,c,g, or c
 / US-09-925-298-245

Query Match 63.8%; Score 1158.6; DB 13; Length 1197;
 Best Local Similarity 99.3%; Pred. No. 5,6e-302;
 Matches 1180; Conservative 3; Mismatches 3; Indels 2; Gaps 2;

DB 624 GCGCTGCTTACTGCTGAGATCAAGCTGCGCCCTGGGCGCATCTCCAGGAGCA 683
 DB 11 GCGCTGCTTACTGCTGAGATCAAGCTGCGCCCTGGGCGCATCTCCAGGAGCA 70

QY 684 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTCAGCAAGCCAGGAGCAATCAAC 743
 Db 71 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTCAGCAAGCCAGGAGCAATCAAC 130
 QY 744 TGACGAGCTTTGAGCTCGCAAGAGTGTATCATAGAGGAGCCGTCACTCAACCTTCT 803
 Db 131 TGACGAGCTTTGAGCTCGCAAGAGTGTATCATAGAGGAGCCGTCACTCAACCTTCT 190
 QY 804 GCGGACCACTTGAATCAATGCCCCCTG-AGATTCTGTGTGCGAGTGGCCACACCGGGCT 862
 Db 191 GCGGACCACTTGAATCAATGCCCCCTG-AGATTCTGTGTGCGAGTGGCCACACCGGGCT 250
 QY 863 GTGAGCTGTGAGAGCTGGGGGCCCCCTATATGTAAGACATGCTCACTGATGATGCGCCCTTT 922
 Db 251 GTGAGCTGTGAGAGCTGGGGGCCCCCTATATGTAAGACATGCTCACTGATGATGCGCCCTTT 310
 QY 923 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATAGAGGAGCAAGTGGACCTGCC 982
 Db 311 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATAGAGGAGCAAGTGGACCTGCC 370
 QY 983 CCCTAAGCTCAACCCAGATGCCCCGGAGACTGTGTAAGAAAGTTTCTGAAGCGGAATCCAGC 1042
 Db 371 CCCTAAGCTCAACCCAGATGCCCCGGAGACTGTGTAAGAAAGTTTCTGAAGCGGAATCCAGC 430
 QY 1043 CAGCGAATGGGGGTGGCCCAAGGGAGTGTGCTGATGTGAGAGACATCCCTTTTCCGG 1102
 Db 431 CAGCGAATGGGGGTGGCCCAAGGGAGTGTGCTGATGTGAGAGACATCCCTTTTCCGG 490
 QY 1103 CACATGAATTTGGAGCGACCTTTCTGGCTGTGGCTGTGGAGCCCTTTCAAGCCCTGTCTG 1162
 Db 491 CACATGAATTTGGAGCGACCTTTCTGGCTGTGGCTGTGGAGCCCTTTCAAGCCCTGTCTG 550
 QY 1163 CAGTCAAGAGAGAGCGTGAAGCAGTTGATACCGGCTTTCACACGCGAGAGCGCCGTGGAC 1222
 Db 551 CAGTCAAGAGAGAGCGTGAAGCAGTTGATACCGGCTTTCACACGCGAGAGCGCCGTGGAC 610
 QY 1223 AGTCTGTATGACACAGCCCTCAAGAGAGTGGCCAAACAGGCTTCTCCGAGCTTCAATAC 1282
 Db 611 AGTCTGTATGACACAGCCCTCAAGAGAGTGGCCAAACAGGCTTCTCCGAGCTTCAATAC 670
 QY 1283 GTGGGCGCGCTGTGCTCTGAGCAGATATGAAGAGGGCTTCTCTCAAGCCCAAGCTGGC 1342
 Db 671 GTGGGCGCGCTGTGCTCTGAGCAGATATGAAGAGGGCTTCTCTCAAGCCCAAGCTGGC 730
 QY 1343 TCACCGAGGCGCTCAACAGTACGCCCCGGGTCCCGTCAAGCCCTCAAGTCTCCCT 1402
 Db 731 TCACCGAGGCGCTCAACAGTACGCCCCGGGTCCCGTCAAGCCCTCAAGTCTCCCT 790
 QY 1403 TTTGAGAGGGTTTGGGCGCAAGCCCAAGCTGTGCGAGAGCCCAAGAGCTTCACTTCA 1462
 Db 791 TTTGAGAGGGTTTGGGCGCAAGCCCAAGCTGTGCGAGAGCCCAAGAGCTTCACTTCA 850
 QY 1463 CTCCTGCAACGCGCGCGCTTGCAGACACGCGCCCTCTCCCATCCGTCCCGCTCAAGG 1522
 Db 851 CTCCTGCAACGCGCGCGCTTGCAGACACGCGCCCTCTCCCATCCGTCCCGCTCAAGG 910
 QY 1523 ACCAAGAGTCCAAAGAGGGGCGGTGGCGCTCAAGGCGCTTGAAGAGCCGGGTGGAGTGA 1582
 Db 911 ACCAAGAGTCCAAAGAGGGGCGGTGGCGCTTGAAGAGCCGGGTGGAGTGA 970
 QY 1583 GGGTGAAGCTTGAAGCCCTGCTGCGGAGCTGAGAGAGAGAGAGAGCCCTGGGCGCAATTC 1642
 Db 971 GGGTGAAGCTTGAAGCCCTGCTGCGGAGCTGAGAGAGAGAGAGAGCCCTGGGCGCAATTC 1030
 QY 1643 AGAGACCTTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGTGATGAAGTGTGTGTCT 1702
 Db 1031 AGAGACCTTGGGGGTGTGTCTGGGGGTGGGGGTGTGAGTGTGATGAAGTGTGTGTCT 1090
 QY 1703 GGGGAGCTGTGCGCCCTGATATCAATGGGAGCGAGAGGGCGCCCGCCCAACCGCGCTCA 1762
 Db 1091 GGGGAGCTGTGCGCCCTGATATCAATGGGAGCGAGAGGGCGCCCGCCCAACCGCGCTCA 1149
 QY 1763 CTGCTCCGTGAAGATTAAGGGCTGAATCATGAAAAAATGAAAAA 1810

Db 1150 CTGCTCCGTGAAGATTAAGGGCTGAATCATGAAAAAATGAAAAA 1197
 RESULT 3
 US-10-102-806-245
 ; Sequence 245, Application US/10102806
 ; Publication No. US2003005421A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: P4103P1
 ; CURRENT APPLICATION NUMBER: US/10/102, 806
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: 09/925, 298
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05881
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124, 270
 ; NUMBER OF SEQ ID NOS: 846
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 245
 ; LENGTH: 1197
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (218)
 ; OTHER INFORMATION: n equals a,t,g, or c
 ; NAME/KEY: misc_feature
 ; LOCATION: (1193)
 ; OTHER INFORMATION: n equals a,t,g, or c
 US-10-102-806-245
 Query Match 63.8%; Score 1158.6; DB 15; Length 1197;
 Best Local Similarity 99.3%; Pred. No. 6,6e-302;
 Matches 1180; Conservative 3; Mismatches 3; Indels 2; Gaps 2;
 QY 624 CGGCGCTTCTTCACTGCTGAGTACAGCTGGCCCTGGGAGCATCCAGAGGCA 683
 Db 11 CGGCGCTTCTTCACTGCTGAGTACAGCTGGCCCTGGGAGCATCCAGAGGCA 70
 QY 684 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTCAGCAAGCCAGGAGCAATCAAC 743
 Db 71 TCATCTACCGGAGCTTCAAGCCCGAGAAATCATATGCTCAGCAAGCCAGGAGCAATCAAC 130
 QY 744 TGACGAGCTTTGAGCTCGCAAGAGTGTATCATAGAGGAGCCGTCACTCAACCTTCT 803
 Db 131 TGACGAGCTTTGAGCTCGCAAGAGTGTATCATAGAGGAGCCGTCACTCAACCTTCT 190
 QY 804 GCGGACCACTTGAATCAATGCCCCCTG-AGATTCTGTGTGCGAGTGGCCACACCGGGCT 862
 Db 191 GCGGACCACTTGAATCAATGCCCCCTG-AGATTCTGTGTGCGAGTGGCCACACCGGGCT 250
 QY 863 GTGAGCTGTGAGAGCTGGGGGCCCCCTATATGTAAGACATGCTCACTGATGATGCGCCCTTT 922
 Db 251 GTGAGCTGTGAGAGCTGGGGGCCCCCTATATGTAAGACATGCTCACTGATGATGCGCCCTTT 310
 QY 923 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATAGAGGAGCAAGTGGACCTGCC 982
 Db 311 ACCGAGAGAACCGGAGAGAAACCATGATTAAGATCATAGAGGAGCAAGTGGACCTGCC 370
 QY 983 CCCTAAGCTCAACCCAGATGCCCCGGAGACTGTGTAAGAAAGTTTCTGAAGCGGAATCCAGC 1042
 Db 371 CCCTAAGCTCAACCCAGATGCCCCGGAGACTGTGTAAGAAAGTTTCTGAAGCGGAATCCAGC 430
 QY 1043 CAGCGAATGGGGGTGGCCCAAGGGAGTGTGCTGATGTGAGAGACATCCCTTTTCCGG 1102
 Db 431 CAGCGAATGGGGGTGGCCCAAGGGAGTGTGCTGATGTGAGAGACATCCCTTTTCCGG 490
 QY 1103 CACATGAATTTGGAGCGACCTTTCTGGCTGTGGCTGTGGAGCCCTTTCAAGCCCTGTCTG 1162

Db 1136 GTGGCCAGGGAGTCTGTATGTGACAGACATCCCTTTTCGGGACATGATGG 1195
Qy 1116 ACGACCTTCTGGCCGCGGTGTGACCCCGCTTTC-AGGCGCTGTGTGACATGACAGAG 1174
Db 1196 ACGA-CTTCTGGCCGCGGTGTGACCCCGCTTTCAGAGGCGCTGTGTGACATGACAGAG- 1253
Qy 1175 GACGTGACCGCATTTGATACCGCTTTCACACGGGACGCGGTGTGACATGCTGATGAC 1234
Db 1254 GACGTGAG-CAGTTTGTATACCGCTTTCACACGGGACGCGGTGTGACATGCTGATGAC 1312
Qy 1235 ACAGCCCTTTCAGAGAGTGTGACACGAGCGCTTTCGCGCTTTCACATGATGCGCGCTT 1294
Db 1313 ACAG-CTTTCAGAGAGTGTGACACGAGCGCTTTCGCGCTTTCACATGATGCGCG-CTCT 1369
Qy 1295 GTCCGTGACAG 1305
Db 1370 GTCCGTGACAG 1380

RESULT 5

US-10-305-720-126
; Sequence 126, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhammer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressio
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 126
; LENGTH: 1607
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040010136A1 1309709
; NAME/KEY: unsure
; LOCATION: (1) ... (1607)
; OTHER INFORMATION: a, t, c, g, or other
US-10-305-720-126

Query Match 39.6%; Score 720; DB 16; Length 1607;
Best Local Similarity 99.1%; Pred. No. 1,1e-183;
Matches 734; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 874 GAGCCTGGGGGCGCTGATGTACGACATGCTCACTGATGCGCGCGCTTTCACCGCAGAGAA 933
Db 868 GCGCTGGGACCGCTGATGTACGACATGCTCACTGATGCGCGCGCTTTCACCGCAGAGAA 927
Qy 934 CCGGAGAAAACCATGATATGATCATGAGGGGCACTGCGCTGCGCTTACCTCTAC 993
Db 928 CCGGAGAAAACCATGATATGATCATGAGGGGCACTGCGCTGCGCTTACCTCTAC 987
Qy 994 CCGGAGTGGCGCGGACCTTGTCAAAAAGTTTGTAAACGGAATCCAGCGAGGATGG 1053
Db 988 CCGGAGTGGCGCGGACCTTGTCAAAAAGTTTGTAAACGGAATCCAGCGAGGATGG 1047
Qy 1054 GGGTGGCCCAAGGGATGCTGTGTGACAGAGCATCCCTTTTCCGACATGATGG 1113
Db 1048 GGGTGGCCCAAGGGATGCTGTGTGACAGAGCATCCCTTTTCCGACATGATGG 1107
Qy 1114 GGAAGACCTTGTGCGCTGTGTGACACCGCGCTTTCAGGCGCTTGTGTGACATGAGAA 1173
Db 1108 GGAAGACCTTGTGCGCTGTGTGACACCGCGCTTTCAGGCGCTTGTGTGACATGAGAA 1167
Qy 1174 GGAAGTGAAGCGATTTGATACCGCTTTCAGCGGACAGCGCGGTGTGACATGATGA 1233
Db 1168 GGAAGTGAAGCGATTTGATACCGCTTTCAGCGGACAGCGCGGTGTGACATGATGA 1227

Qy 1234 CAGACCTTTCAGAGAGTGTGACACGAGCGCTTCTGTGGCTTTCATATGCTGGCGCTC 1293
Db 1228 CAGACCTTTCAGAGAGTGTGACACGAGCGCTTCTGTGGCTTTCATATGCTGGCGCTC 1287
Qy 1294 TGTCTGACAGCATCAGAGAGGCGCTTCTTTCAGAGCGCAAGCTGCGCTCACCGAGCG 1353
Db 1288 TGTCTGACAGCATCAGAGAGGCGCTTCTTTCAGAGCGCAAGCTGCGCTCACCGAGCG 1347
Qy 1354 CTTCACATGATGAGCGCGCGGTGTGACACCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1413
Db 1348 CTTCACATGATGAGCGCGCGGTGTGACACCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1407
Qy 1414 TCGAGCCAGCGCGCGAGCTGTGACAGCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1473
Db 1408 TCGAGCCAGCGCGAGCTGTGACAGCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1467
Qy 1474 GCGCGCGCGCTTTCAGAGCGCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1533
Db 1468 GCGCGCGCGCTTTCAGAGCGCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1527
Qy 1534 CAGAGAGGCGCGGTGTGACAGAGCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1593
Db 1528 CAGAGAGGCGCGGTGTGACAGAGCGCGCTTTCAGAGCGCAAGCTTTCAGAGCG 1586
Qy 1594 GAGCCTGTCTCTGCGCGCTGT 1614
Db 1587 GAGCCTGTCTCTGCGCGCTGT 1607

RESULT 6

US-09-968-433-58
; Sequence 58, Application US/09968433
; Publication No. US20030073162A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn B.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PC-0051 CIP
; CURRENT APPLICATION NUMBER: US/09/968,433
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PERL Program
; SEQ ID NO 58
; LENGTH: 1058
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030073162A1 037196_Mm.1
US-09-968-433-58

Query Match 37.0%; Score 672.6; DB 10; Length 1058;
Best Local Similarity 89.7%; Pred. No. 5.8e-171;
Matches 745; Conservative 0; Mismatches 84; Indels 2; Gaps 2;

Qy 86 GGCCTGAGCGGCG 145
Db 48 GGCCTGAGCGGCG 107
Qy 146 ACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 205
Db 108 ACGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 167
Qy 206 CTTCGCGAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 265
Db 168 CTTCGCGAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 227
Qy 266 ACTGAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 325

Db 228 ACAGAGACAGCGTGAACCTGGGTCTGAGCGCATCGGCCCCACTGCTTGAAGCTACTG 287
Qy 326 CGTGTGCTGGGCAAGGGGGGCTATAGCAAGGTGTTCAGAGTCCGAAGGTGCAAGGACC 385
Db 288 AGTGTACTGGGCAAGGGGGGCTATAGCAAGGTGTTCAGAGTCCGAAGGTGCAAGGACC 347
Qy 386 AACTTGGGCAAAATATATATGCTATGCAAGGTGTTCAGAGTCCGAAGGTGCAAGGACC 445
Db 348 AACTTGGGCAAAATATATATGCTATGCAAGGTGTTCAGAGTCCGAAGGTGCAAGGACC 407
Qy 446 AAGGACACAGACACACAGGCGCTGAGCGGAACCTTATAGTCAAGGAAAGCAACCCCTT 505
Db 408 AAGGACACAGGCGCTGAGCGGAACCTTATAGTCAAGGAAAGCAACCCCTT 467
Qy 506 ATTGTGAACTGGCTATGCTTTCAGACTGTGCGCAACTCTACCTCATCTTGAAGTGC 565
Db 468 ATTGTGAACTGGCTATGCTTTCAGACTGTGCGCAACTCTACCTCATCTTGAAGTGC 527
Qy 566 CTCAGTGTGGCGAGCTCTTCAGCATCTGAGAGGAGGCACTTCTCTGAAAGTACG 625
Db 528 CTCAGTGTGTGGCTCTTCAGCATCTGAGAGGAGGCACTTCTCTGAAAGTACG 587
Qy 626 GCTGCTTCTACCTGCTGAGATCAAGCTGGGCGCTGAGCGCACTCCAGGCGATC 685
Db 588 GCTGCTTCTACCTGCTGAGATCAAGCTGGGCGCTGAGCGCACTCCAGGCGATC 646
Qy 686 ATCTACCGGACCTCAAGCCCGAGACATATGCTGAGAGCGGCGCACTCAAACTG 745
Db 647 ATCTACCGGACCTCAAGCCCGAGACATATGCTGAGAGCGGCGCACTCAAACTG 706
Qy 746 ACCGACTTGGACTCTGAGAGAGTCTATCAAGAGGCGCGCTCACTGACCTTCTG 805
Db 707 ACGACTTGGACTCTGAGAGAGTCTATCAAGAGGCGCGCTCACTGACCTTCTG 766
Qy 806 GCGACCATTTAGTACATGAGCCCTGAGA-TTCTGTGTCGCGAGTGGCCCAACCGGCTGT 864
Db 767 GCGACCATTTAGTACATGAGCCCTGAGA-TTCTGTGTCGCGAGTGGCCCAACCGGCAAGT 826
Qy 865 GAGCTGTGAGGCTGGGGGCGCTGATGTGAGACATCTCATCTGATCGGC 915
Db 827 GAGCTGTGAGGCTGGGGGCGCTGATGTGAGACATCTCATCTGATCGGC 877

RESULT 7
US-10-316-253-31
; Sequence 31, Application US/10316253
; Publication No. US20030162706A1
; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865K
; CURRENT APPLICATION NUMBER: US/10/316,253
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 1800
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (114)..(1642)
; OTHER INFORMATION:
US-10-316-253-31

Query Match 34.6%; Score 628.8; DB 15; Length 1800;
Best Local Similarity 71.1%; Pred. No. 4,1e-159;

Matches 831; Conservative 0; Mismatches 337; Indels 0; Gaps 0;
Qy 240 TGGGACATATGAAAGGTGAGCTGACATGACACCGCTGAACTTTGGCCCAAGACGCA 299
Db 261 TGGAACTATTTGAAATTTGAAATCTGAAATCTGAAATCTGAAATCTGAAATCTGAA 320
Qy 300 TGGGCCCCAGCTTTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
Db 321 TGAACCAAGATGTTTGAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 380
Qy 360 TCCAGTGGGAAAGGTGCAAGGACCAACTTGGGCAAAATATATGCAAGGAAAGTCTTA 419
Db 381 TCCAGTGGGAAAGGTGCAAGGACCAACTTGGGCAAAATATATGCAAGGAAAGTCTTA 440
Qy 420 GGAAGGCAAAATTTGCGCAATGCGGAGACAGACACACACGCGCTGAGCGGAGCA 479
Db 441 AAGGCAATGATGATGAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 500
Qy 480 TTCTAGAGTCAAGTGAAGCAACCTCTTATTTGGAAGTGGCTTATGCTTCCAGCTGTG 539
Db 501 TTCTAGAGTCAAGTGAAGCAACCTCTTATTTGGAAGTGGCTTATGCTTCCAGCTGTG 560
Qy 540 GCAAACTTACCTCATCTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 599
Db 561 GAAACTTCACTTCACTTGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 620
Qy 600 GAGAGGCAATCTTCTGGAAGTGAAGGCGCTGCTTCTACCTGCTGAGATCAAGTGGCC 659
Db 621 GAGAGGCAATCTTCTGGAAGTGAAGGCGCTGCTTCTACCTGCTGAGATCAAGTGGCC 680
Qy 666 TGGGCGATCTGACCTCCGCGCATCATCTACCGGAGCTCAAGCCCGAGACATATG 719
Db 681 TGGGCGATCTGACCTCCGCGCATCATCTACCGGAGCTCAAGCCCGAGACATATG 740
Qy 720 TCGAGAGCGGCGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 779
Db 741 TTAATCAACCAAGTCAAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 800
Qy 780 AAGGCGCGCTGACCTGACCTGCTGCGGACCAATTGAGTGAAGTGGCCCTGAGATTCTG 839
Db 801 ATGGAACAGTCAAGCAATTTTGTGAACATATGAATATGAGTGGCCCTGAGATTCTG 860
Qy 840 TCGGAGTGGCCCAACCGGCTGAGCTGTGAGAGCTGGGCGCCCTGAGTGAAGCA 899
Db 861 TGAAGAGGCGCAACCGGCTGAGCTGTGAGAGCTGGGCGCCCTGAGTGAAGCA 920
Qy 900 TCTCACTGAGATGCGCGCTTACCGGAGAGACCGGAAACCAATGATTAAGTCA 959
Db 921 TCTCACTGAGATGCGCGCTTACCGGAGAGACCGGAAACCAATGATTAAGTCA 980
Qy 960 TCAAGGCGCAAGCTGAGCTGCGCCCTTACCTGACCCGAGATGCGCGGACTTGTCAAA 1019
Db 981 TCAAGTGAATTAATTTTGTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1040
Qy 1020 AGTTTCTGAACGAAATCCAGCGAGATTTGGGGTGGCCCAAGGATGCTGCTGATG 1079
Db 1041 AGTTTCTGAACGAAATGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1100
Qy 1080 TGCAGAGACCTCTTTTCCGCGACATGAATTTGGGAGGACCTTGTGCTGCTGCTG 1139
Db 1101 TGCAGAGACCTCTTTTCCGCGACATGAATTTGGGAGGACCTTGTGCTGCTGCTG 1160
Qy 1140 ACCGCTCTTCAAGCGCTGCTGCAAGTGAAGAGAGAGTGAAGCGGATTTATCCGCT 1199
Db 1161 AGCGCTCTTCAAGCGCTGCTGCAAGTGAAGAGAGAGTGAAGCGGATTTATCCGCT 1220
Qy 1200 TCAAGCGGAGAGCGGCTGAGAGTCTGATGACAGAGCTTCAAGAGTGAAGTGAAG 1259
Db 1221 TTAAGTCTGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1280
Qy 1260 AAGGCTTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1319
Db 1281 AAGTCTTCTGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 1340

QY 1320 TCTCTTCCAGGCGCAAGTGTGAGTCCAGGCGCTCAAGATGATGCGGCTCCCG 1379
 DB 1341 TTTCTTTGAGACCAAAATCCGATGCTCGAAATTTATGTGAGCCCAAGACGCTG 1400
 QY 1380 TCAGCCCTCAAGTCTCCCTTTTGA 1407
 DB 1401 TCAGCCAGTCAAAATCTCTCTGGGGA 1428

RESULT 8

US-10-316-253-33
 ; Sequence 33, Application US/10316253
 ; Publication No. US20030162706A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Procter & Gamble Company
 ; APPLICANT: Petere, Kevin
 ; APPLICANT: Thompson, Larry
 ; APPLICANT: Wang, Feng
 ; APPLICANT: Greis, Kenneth
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins
 ; FILE REFERENCE: 8865M
 ; CURRENT APPLICATION NUMBER: US/10/316,253
 ; PRIOR FILING DATE: 2002-12-10
 ; PRIOR APPLICATION NUMBER: US 60/355,295
 ; NUMBER OF SEQ ID NOS: 308
 ; SOFTWARE: Patent version 3.1
 ; SEQ ID NO 33
 ; LENGTH: 2287
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (22)..(1599)
 ; OTHER INFORMATION:
 US-10-316-253-33

Query Match 34.6%; Score 628.2; DB 15; Length 2287;
 Best Local Similarity 71.1%; Pred. No. 6,36-159;
 Matches 830; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

QY 240 TGGGACATAAGAGAGTGTGAGTGAAGACAGAGGGAAGCTTGGCCCGAGAGGCA 239
 DB 218 TGGAACTTGTGAAATTTGAAATCTCAAGAACTAGTGAACAGAGGCGCAAGAAAA 277
 QY 300 TCGGCCCCCACTGCTTGAAGCTGTGCTGTGTGTGTGAGCAAGGGGGCTATGCAAGGTGT 359
 DB 278 TCAGACCAGATGTTTGAAGTACTTCTGGGTAATGTGTAAGGGGGCTATGGAAGGTTT 337
 QY 360 TCCAGGTGCGAAGGTGCAAGGCGCAACTTGGCCAAATATATGCAATGAAGTCTTA 419
 DB 338 TTTCAAGTACGAAAGTAACAGAGCAATCTGGGAAGATTTTGCATTAAGGTGCTTA 397
 QY 420 GGAAGCCAAATTTGTGCGATATCCCAAGACACAGACACACACAGGCTGAGCGGACA 479
 DB 398 AAAAGGCAATGATGTAAAGAAATGCTAAGTACAGTCAATCAAAAGCAGAGGGAAAT 457
 QY 480 TTCTAGTGTGAGAGACACCCCTTTATTTGTGAACTGCGCTTATGCTTCAAGCTGTG 539
 DB 458 TTTCTGAGAGATTAACATCTCTTCAATTTGATTTAATTTATTTGCTTTCAACCGGTG 517
 QY 540 GCAAACTTACCTTATCTTGAAGTCTCAGTGTGCGAGCTTTCACGATCTGGAGC 599
 DB 518 GAAAGCTTACCTTATCTTGAAGTCTCAGTGTGCGAGCTTTCACGATCTGGAGC 577
 QY 600 GAGAGGCAATCTTCTGGAAGATACGGCTGCTTCTTACCTGCTGAGATCAAGCTGGCC 659
 DB 578 GAGAGGCAATCTTCTGGAAGATACGGCTGCTTCTTACCTGCTGAGATCAAGCTGGCC 637
 QY 660 TGGGCAATCTTCACTCCCAAGGATCATCTACCGGAGCTCAAGCCCGAAGATCATATG 719
 DB 638 TGGGCAATCTTCACTCCCAAGGATCATCTACCGGAGCTCAAGCCCGAAGATCATATG 697

QY 720 TCAGAGCCAGGSCCAATCAAACTGACCGACTTTTGTGACTCTGCAAGAGTCTATTCATG 779
 DB 698 TTTATACCAAGGTCTACGTAAAGCTGACAGACTTTGATCATTAAGAAATCTATTCATG 757
 QY 780 AGGCGCGGCACTTCAACCTTCTGAGGAGCACTATGAGTATCATGAGCCCTGAGATTTG 839
 DB 758 ATGGAACAGTCAAGCACTTTTGTGAGCAATTAATTAATTAATTAATTAATTAATTA 817
 QY 840 TGGCAGTGTGCAAAACCGGCTGTGAGCTGTGAGAGCTTGGGCGCTGATGTACACA 899
 DB 818 TCAGAAAGGCGCAACCGGCTGTGAGATTTGAGAGCTTGGAGCAATTAATGTATGACA 877
 QY 900 TGTCACTGTGATGCGGCGCTTTTACCGGAGAAACCGGAAGAAACCAATGATTAAGTCA 959
 DB 878 TGTGACTGTGAGCACTTCAATCACTGGGAGATTAAGAAAGAAACCAATTAAGCAAAATTC 937
 QY 960 TCAGGGGCAAGTGTGAGCTGCGGCTTCACTCAACCCAGATGCGCGGACCTTGTCAAAA 1019
 DB 938 TCAATGTAAATTAATTTGCTCTTCACTCAACAGAGCTCGAGATCTGCTTAAA 997
 QY 1020 AGTTTCTGAAACGAATCCAGCAAGCAATTTGGGCTGCGGAGATGCTGTGATG 1079
 DB 998 AGCTGTGAAAGAAATGCTGCTTCTGCTGTGAGAGCTGCGGAGATGCTGTGAGAG 1057
 QY 1080 TGCAGAGACATCTCTTTTCCGCAATGATGAGACACTTGTGCGCTGCGGCTGTG 1139
 DB 1058 TCAGAGGCAATCAATTTTATGACATTAATCTGGAAGAGCTTTTGGCTGGAAGTGG 1117
 QY 1140 ACCCTCTTCAAGGCGCTGTGAGTCAAGAGAGAGAGTGAAGCTTGTATACCGCT 1199
 DB 1118 AGGCGCTTGAAGCTCTGTGCAATCTGAAGAGATGAGTCAAGTTGATCAAGT 1177
 QY 1200 TCACAGGAGAGAGCGGCTGTGAGCAATCTGATGACACAGCCCTCAGCGAGAGTGAAC 1259
 DB 1178 TTTACTGTGAGACACTTGTGAGAGCCCGATGATCACTCAATGTGAAGAGTGAAC 1237
 QY 1260 AGGCTCTTCTGAGCTTCAATGAGTGTGAGGAGTGTCTGTCTGTGACAGATCAAGAGGCT 1319
 DB 1238 AGGCTCTTCTGAGCTTCAATGAGTGTGAGGAGTGTCTGTCTGTGACAGATCAAGAGGCT 1297
 QY 1320 TCTCTTCCAGGCGCAAGCTGAGGCTGACCCAGGCGCTCAAGTATGCCCCGCTCCCG 1379
 DB 1298 TTTCTTTGACCAAAATCCATGCTGGAAGATTTATGTGAGCCCAAGACCGCTG 1357
 QY 1380 TCAGCCCTCAAGTCTCCCTTTTGA 1407
 DB 1358 TCAGCCAGTCAAAATCTCTCTGGGGA 1385

RESULT 9

US-10-191-803-230
 ; Sequence 230, Application US/10191803
 ; Publication No. US20040014040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MENDRICK, Donna
 ; APPLICANT: PORTER, Mark
 ; APPLICANT: JOHNSON, Kory
 ; APPLICANT: HIGGS, Brandon
 ; APPLICANT: CASTLE, Arthur
 ; APPLICANT: BLASHOFF, Michael
 ; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
 ; FILE REFERENCE: 44921-5090US
 ; CURRENT APPLICATION NUMBER: US/10/191,803
 ; PRIOR FILING DATE: 2002-07-10
 ; PRIOR APPLICATION NUMBER: US 60/303,819
 ; PRIOR FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: US 60/305,623
 ; PRIOR FILING DATE: 2001-07-17
 ; PRIOR APPLICATION NUMBER: US 60/369,351
 ; PRIOR FILING DATE: 2002-04-03
 ; PRIOR APPLICATION NUMBER: US 60/377,611
 ; PRIOR FILING DATE: 2002-05-06

; NUMBER OF SEQ ID NOS: 1140
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 230
 ; LENGTH: 2287
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031985
 US-10-191-803-230

Query Match 34.6%; Score 628.2; DB 16; Length 2287;
 Best Local Similarity 71.1%; Pred. No. 6,3e-159;
 Matches 83; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

QY 240 TGGGACCTATGAGAGGTGGAGCTGACGAGCAGCGTGAAGCTTGGCCGAGAGCGCA 299
 DB 218 TGGAGACCTGTGAGAAATTTGAAATCTCAAGAACTAGTGTGAACAGAGGCCAGAAAAA 277
 QY 300 TCGGGCCCACTGCTTTGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 359
 DB 278 TCGAGCCAGAAATGTTTGTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCTTCTTCTGCT 337
 QY 360 TCGAGGTGCGAAAGGTGCGAAGCAACCACTTGGGCAAAATATATGTCATGAAAGTCTTA 419
 DB 338 TCGAAGTACGAAAGTACAGAGCAAAATCTGGAAAGATATTTGCCATGAAAGTCTTA 397
 QY 420 GGAAGGTCAAATTTGTGCGAATGCCAGAGCAGACAGCAGCAGCAGCAGCAGCAGCAGC 479
 DB 398 AAAAGGTAAATGATGAGAAAGTCTAAAGATCACTCAATCAAAAGCAGAGCGGAAAT 457
 QY 480 TTCTAGAGTGAAGAGCAACCCCTTTATGTGGAAGTGGCTTAATGCTTCCAGACTGTG 539
 DB 458 TTCTGAGAGAGTAAAGCAATCCCTTCACTGTGATTTAATTAATGCTTCCAGACCGTG 517
 QY 540 GCAAACTTACCTCTATCTTGAAGTCTCACTGTGCGAGCTTCTTCAAGCATCTGAGAC 599
 DB 518 GAAATCTTACCTCACTCTTGAAGTCTCACTGTGCGAGCTTCTTCAAGCATCTGAGAC 577
 QY 600 GAGAGGCACTCTCTGGAAGATACGAGCTGCTTCTACCTGCTGAGTCAAGCTGAGCC 659
 DB 578 GAGAGGCAATTTCAAGAGATACAGCTTCTTCTTCTGCTGAGTCAAGCTGAGCC 637
 QY 660 TGGGCACTCTCTCTGAGAGGATCATCTTACCGGAGCTCAAGCCCGAGAACTATGCT 719
 DB 638 TGGGCACTTCTCTCAAGAGGATCATCTTACCGGAGCTCAAGCCCGAGAACTATGCT 697
 QY 720 TCAAGAGCCAGGCAATCAACTGACGAGCTTGTGAGCTGTGCAAGAGTCTATCATG 779
 DB 698 TTAATCAAGAGTCAAGTGAAGCTTGTGAGCTTGTGAGCTGTGCAAGAGTCTATCATG 757
 QY 780 AGGAGCCGCTCACTCAACCTTGTGCGGACCAATGAGTACATGCTGAGATTTCTG 839
 DB 758 ATGGAACAGTCAAGCACTTTTGTGAACAATTAATATGAGCCCTGAAATTTCTGA 817
 QY 840 TGGGCACTGCGCAACCGGCTGTGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 899
 DB 818 TGGGCACTGCGCAACCGGCTGTGAGCTGTGAGGCTGTGAGGCTGTGAGGCTGTGAGG 877
 QY 900 TGGTCACTGATGCGCGCTTTACCGCAGAGAACCGAGAAACCATGATTAAGATCA 959
 DB 878 TGGTCACTGATGCGCGCTTTACCGCAGAGAACCGAGAAACCATGATTAAGATCA 937
 QY 960 TCGAGGCGCAAGCTGAGCACTGCGCGCTTCACTCAAGCAGATGCGCGGAGCTTGTCAAA 1019
 DB 938 TCGAATGTAATTAATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 997
 QY 1020 AGTTTCTGAAACGAAATCCAGCAGCGAATGGGGGTGGCCAGAGGAATGCTGTGATG 1079
 DB 998 AGCTGTGAAAGAAATGCTGCTTCTGCTTGTGAACTGCGCTGTGGAATGCTGTGAAG 1057
 QY 1080 TGAAGAGATCCCTTTTCCGGAATGAAATTTGGAGCAACCTTCTGCTGCTGCTGCTG 1139
 DB 1058 TCGAAGCGATCCATTTTGAACATTAATCTGGAGAGGCTTTTGTGCTTGGAAAGGTG 1117

QY 1140 ACCCCCTTTGAGGCTCTGAGTCAAGAGAGAGTGAAGCCAGTTTGAATACCGCT 1199
 DB 1118 AGCGCCCTTTAAGCTGTGTTGCAATCTGAAGAGAGATGTGAGTGAATTTGAATCAAGT 1177
 QY 1200 TCAACGCGAGACCGCGGTGAGCACTCTGATGACAGACCTTCAAGAGATGCGCAAC 1259
 DB 1178 TTAATCTGTCAGACACTGTGTGACAGCCCGAGTCACTCACTGATGAAATGCGCAAC 1237
 QY 1260 AGGCTTCTGAGCTTCAATATGAGGCGCTGTGCTGTGCTGTGAGACAGATCAAGAGAG 1319
 DB 1238 AGCTTCTTCTGCTTTCATATGAGTCTCATCTGATTTGAAAGTGAAGAAAGT 1297
 QY 1320 TCTCTTCCAGCCCAAGCTGTGCTCAACCGAGCGCTCAACATGAGTACCGCGGCTCCG 1379
 DB 1298 TTTCTTTTGAACCAAAATTCGATGCTCGAAGATTAATGTGAGCCCAAGAGCTTG 1357
 QY 1380 TCAAGCCCTCAAGTCTCCCTTTGA 1407
 DB 1358 TCAAGCCCAATTTCTCTCTGAGGA 1385

RESULT 10
 US-09-954-456-1137
 ; Sequence 1137, Application us/09954456
 ; Patent No. US20020115057A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Paul
 ; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
 ; FILE REFERENCE: 689290-76
 ; CURRENT APPLICATION NUMBER: US/09/954,456
 ; PRIOR FILING DATE: 2001-09-18
 ; PRIOR APPLICATION NUMBER: US/60/233,617
 ; PRIOR FILING DATE: 2000-09-18
 ; PRIOR APPLICATION NUMBER: US/60/234,052
 ; PRIOR FILING DATE: 2000-09-20
 ; PRIOR APPLICATION NUMBER: US/60/234,923
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,134
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: US/60/235,637
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,638
 ; PRIOR FILING DATE: 2000-09-26
 ; PRIOR APPLICATION NUMBER: US/60/235,711
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,720
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,840
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US/60/235,863
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 2276
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO 1137
 ; LENGTH: 2346
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-954-456-1137

Query Match 34.1%; Score 619.8; DB 9; Length 2346;
 Best Local Similarity 70.5%; Pred. No. 1.2e-156;
 Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;

QY 240 TGGACACTATGAAAGGTGAGGCTGACTGAGACCAAGCTGAACGTTGGCCGAGAGCGCA 299
 DB 224 TGAACATTTGAGAAATTTGAAATCTCAAGAACTAGTGTGAACAGAGGCGCAGAAAAA 283
 QY 300 TCGGCGCCCACTGCTTTGAGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 359
 DB 284 TGAACCAAGATTTTGAAGTCTTCTGAGTCTGAGTCTTGTGTAAGAGGCGCTATGAAAGT 343

QY 360 TCACGCTGCAAGAGTGCAGAGCCAACTTGGGCAAAATATATGCCATGAAATCTCTAA 419
 Db 344 TTCAAGTACGAAAGATACAGAGCAAAATACCTGGGAAATATTTGCCATGAAAGCTGCTTA 403
 QY 420 GGAAGGCAAAATATGTCGCAATGCAAGACACAGGCAACACCGGCTGAGGGGACA 479
 Db 404 AAAAGGCATATATATTAAGAAATGCTAAAGATACAGCTCATACAAAAGCAAGCAAGATA 463
 QY 480 TTCTAGAGTCAAGTAAAGCAACCTTTATTTGGAATCGGCTATGCTTCAGATGATG 539
 Db 464 TTCTGAGAGAGTAAAGCATCCCTTCATCGTGAATTTATTTATGCTTCAGATGATG 523
 QY 540 GCAAACTTACCTATCTTGAAGTCTTGAAGTCTGAGTGTGAGTCTTCAAGCATTTGAGC 599
 Db 524 GAAACTTACCTATCTTGAAGTCTTGAAGTCTGAGTGTGAGTCTTCAAGCATTTGAGC 583
 QY 600 GAGAGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 659
 Db 584 GAGAGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 643
 QY 660 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 719
 Db 644 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 703
 QY 720 TCACAGCAGAGGCAATCAATCAAACTGAACGACTTGAAGTGTGAGTGTGAGTGTGAGC 779
 Db 704 TTAATCAACAGGCAATCAATCAAACTGAACGACTTGAAGTGTGAGTGTGAGTGTGAGC 763
 QY 780 AGGAGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 839
 Db 764 ATGGAAGTCAACACACATTTTGTGAACAAATGAAATGAAATGAAATGAAATGAAATG 823
 QY 840 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 899
 Db 824 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 883
 QY 900 TGGTCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 959
 Db 884 TGGTCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 943
 QY 960 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 1019
 Db 944 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 1003
 QY 1020 AGTTTCTGAAGAGGCAATCCAGAGGCAAGTGGGGGCTGGCCAGGGGAGTGTGAGTGTG 1079
 Db 1004 AGTGTCTGAAGAGGCAATCCAGAGGCAAGTGGGGGCTGGCCAGGGGAGTGTGAGTGTG 1063
 QY 1080 TGAAGAGCATCTCTTTTTCGGGCAATGAATTTGGAAGCACTTGTGGCTGGCTGTGAG 1139
 Db 1064 TTAAGAGCATCTCTTTTTCGGGCAATGAATTTGGAAGCACTTGTGGCTGGCTGTGAG 1123
 QY 1140 ACCGCTTCTGAGGCTGTGTCAGTCAAGTCAAGAGGAGTGTGAGTGTGAGTGTGAGC 1199
 Db 1124 AGCGCTTCTGAGGCTGTGTCAGTCAAGTCAAGAGGAGTGTGAGTGTGAGTGTGAGC 1183
 QY 1200 TCAAGAGGCAAGGCTGTGTCAGTCAAGTCAAGAGGAGTGTGAGTGTGAGTGTGAGC 1259
 Db 1184 TTAAGAGGCAAGGCTGTGTCAGTCAAGTCAAGAGGAGTGTGAGTGTGAGTGTGAGC 1243
 QY 1260 AGGCTTCTGAGGCTGTGTCAGTCAAGTCAAGAGGAGTGTGAGTGTGAGTGTGAGC 1319
 Db 1244 AGGCTTCTGAGGCTGTGTCAGTCAAGTCAAGAGGAGTGTGAGTGTGAGTGTGAGC 1303
 QY 1320 TCTCTCTCAAGGCTGTGTCAGTCAAGAGGAGTGTGAGTGTGAGTGTGAGTGTGAGC 1379
 Db 1304 TTTCTTTTGAACCAAAATCCGATTCAGTCAAGTGTGAGTGTGAGTGTGAGTGTGAGC 1363
 QY 1380 TCAAGGCTTCTCAAGTGTCTCCCTTTTGA 1407
 Db 1364 TCAAGGCTTCTCAAGTGTCTCCCTTTTGA 1391

RESULT 11
 US-09-920-677-3
 ; Sequence 3, Application US/09920677
 ; Publication No. US20030083284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bret P. Monia
 ; APPLICANT: Lex M. Cowart
 ; TITLE OF INVENTION: ANTISENSE MODULATION OF P70 S6 KINASE EXPRESSION
 ; FILE REFERENCE: RTS-0245
 ; CURRENT APPLICATION NUMBER: US/09/920,677
 ; CURRENT FILING DATE: 2001-08-01
 ; NUMBER OF SEQ ID NOS: 43
 ; SEQ ID NO 3
 ; LENGTH: 2346
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (28)...(1605)
 US-09-920-677-3
 Query Match 34.1%; Score 619.8; DB 10; Length 2346;
 Best Local Similarity 70.5%; Pred. No. 1,2e-156;
 Matches 824; Conservative 0; Mismatches 344; Indels 0; Gaps 0;
 QY 240 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 299
 Db 224 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 283
 QY 300 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 359
 Db 284 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 343
 QY 360 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 419
 Db 344 TTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 403
 QY 420 GGAAGGCAAAATATGTCGCAATGCAAGACACAGGCAACACCGGCTGAGGGGACA 479
 Db 404 AAAAGGCATATATATTAAGAAATGCTAAAGATACAGCTCATACAAAAGCAAGCAAGATA 463
 QY 480 TTCTAGAGTCAAGTAAAGCAACCTTTATTTGGAATCGGCTATGCTTCAGATGATG 539
 Db 464 TTCTGAGAGAGTAAAGCATCCCTTCATCGTGAATTTATTTATGCTTCAGATGATG 523
 QY 540 GCAAACTTACCTATCTTGAAGTCTTGAAGTCTGAGTGTGAGTCTTCAAGCATTTGAGC 599
 Db 524 GAAACTTACCTATCTTGAAGTCTTGAAGTCTGAGTGTGAGTCTTCAAGCATTTGAGC 583
 QY 600 GAGAGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 659
 Db 584 GAGAGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 643
 QY 660 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 719
 Db 644 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 703
 QY 720 TCACAGCAGAGGCAATCAATCAAACTGAACGACTTGAAGTGTGAGTGTGAGTGTGAGC 779
 Db 704 TTAATCAACAGGCAATCAATCAAACTGAACGACTTGAAGTGTGAGTGTGAGTGTGAGC 763
 QY 780 AGGAGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 839
 Db 764 ATGGAAGTCAACACATTTTGTGAACAAATGAAATGAAATGAAATGAAATGAAATG 823
 QY 840 TGGGCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 899
 Db 824 TGAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGC 883
 QY 900 TGGTCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 959
 Db 884 TGGTCAATCTTCTGGAAGATAGGAGCTGCTTCAAGTGTGAGTGTGAGTGTGAGC 943

QY	960	TCAGGGGCAAGTGGACATCCACCCCTTACCTGACACCCGAGATGACCCTGGACCTTGGCAAA	101.9
Db	944	TCAAATGTAAACTCAATTTCCTCTCTTACTACACAGAAAGCCAGAAATCTGCTTAAA	100.3
QY	1020	AGTTTCTGAAACGGAATCCCAAGCAGCGGAATGGGAGTGGCCCAAGGGAATGCTGTATG	107.9
Db	1004	AGCTGCTAAGAAAGAAATGCTGCTTCTCTGAGAGCTGATCTTGGGAGCCCTGGAGAG	106.3
QY	1080	TGCATGACATCCCTTTTTCGGGCAATGAAATTTGGAGAGACTTCTGTGGCCGTGGCTGAG	113.9
Db	1064	TTCAAGCTCATTCATTCTTTTAAACATATTAAGTGGAAAGAACTTGTGCTGAAAGGTGG	112.3
QY	1140	AACCCCTTTGAGGCGCTGTCTGACATGAGAGAGAGACGTGAGCCAGTTTAAATCCGCT	119.9
Db	1124	AGCCCCCTTTAAACTCTGTTGGCAATGTAAAGAGAAATGAAGTCAAGTTTGAATTCAGT	118.3
QY	1200	TCACACGGGCAAGCCCGGTGGACAGTCTGATGACACAGCCCTCAGCGAGATGCGCAAC	125.8
Db	1184	TTACACGTCAAGACATCTGTGACAGACCCAGATGATCTCAACTCAGTAAAGTGGCAATC	124.3
QY	1260	AGGCTTCTGTGGGCTTCACATACGTGGCGCCGCTGTCTCTGGAACGATCAAGAGGGCT	131.9
Db	1244	AGGTCCTTCTGGGTTTACATATGAGTGGCTTCATCTGTACTTGAAGTGTGAAAGAAAAGT	130.3
QY	1320	TCTCTCTTCAGCCCAAGCTGGGCTCACCCAGGCGCTCAACAGTAAGCCCGGGTCCCG	137.9
Db	1304	TTTCTCTTGAACCAAAATTCGATCACTTCGAAGATTTATTATGGACGCCCAAGAACCTG	136.3
QY	1380	TCAGGCCCCCAAGTTCCTCCCTTTTGA	140.7
Db	1364	TCAGGCCAGTCAAAATTTCTCTGGGGA	139.1

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RESULT 12
US-10-388-360-321
; Sequence 321, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
; APPLICANT: GENOMIC HEALTH
; APPLICANT: Baker, Joffie B.
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Shak, Steve
; APPLICANT: Walker, Michael Graham
; TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
; FILE REFERENCE: 39740-0001US
; CURRENT APPLICATION NUMBER: US/10/388,360
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/412,049
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US 60/364,890
; PRIOR FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 384
; SOFTWARE: fastseq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 2346
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-388-360-321

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Query Match	34.1%;	Score 619.8;	DB 13;	Length 2346;
Best Local Similarity	70.5%;	Pred. No. 1.2e-156;		
Matches 824;	Conservative 0;	Mismatches 344;	Indels 0;	Gaps 0;

QY	240	TGGGACCATGAAAGGTGGAGCTGACTGAGACCAAGGTGAACGTTGGCCGAGACGCA	299
Db	224	TGGAACTATTGTGAAATTTTGAATCTCAGAAACTAGTGTGACAGAGGGCCAGAAAAA	283
QY	300	TCCGGCCCACTGCTTTAGAGTCGTCGCGGTGCTCGGCAAGGGGGCTTAGCGCAAGTGT	359
Db	284	TCCGACCCAGATGTTTGTAGTCACTTGGGATCTTGTGAAAGGGGGGCTTAGGAAAGGTTT	343
QY	360	TCCAGGTGCAGAAAGTGCAGGCAACCACTGGGGCAAAATATATGCATGAAGTCTTAA	419

Db	344	TTCAAGTACGAAAAAGTAA	CAGAGCAAAATAC	TGGGAAAAATATTTGGCCATGAAAGTGCCTTA	403
Qy	420	GGAAGGCCAAATTTGTGCGCAATG	CCAGACACACAGCACACACACGCGCTBAGCGGAA	479	
Db	404	AAAAGGCATGATGTATGAAGATG	CTAAAGATACAGCTCATACAAAGCAGAGCGAATA	463	
Qy	480	TTCTAGAGTCAGTGAAGACACC	CTTTATTTGTGGAAC	TGGCCCTATGCTCTTCAGACTGTG	539
Db	464	TTCTGGAGGAAGTAAAGCATCC	CTTCATCGTGGATTAAATTTATG	CCCTTCAGACTGGTG	523
Qy	540	GCAACTCTTACTCATCTCTTAA	GTGCGCCATGTGTGGAGACTCTTCA	ACGATCTGAGC	599
Db	524	GAATACTTACTCTCACTTAA	GTATCTCAATGTGAAGAGAACTATTTATG	CAGTTAGAA	583
Qy	600	GAGAGGAGCATCTTCTGTGA	AGATAACGACTGTCTTCTA	CTGGCTGAGATCAACGCTGCGCC	659
Db	584	GAGAGGGAATTTTATGGAG	ACATCTGCTCTTTTACTTGGCAGAAATCTC	ATGCGCTT	643
Qy	660	TGGCGCATCTCCATCTCC	AGGGACATCATACCGGGACCTCA	AGCCCGAGACATCATG	719
Db	644	TGGGCGATTTATCATCAAA	AGGGAATCATCTACAGACCTTA	AGCCGAGAAATTCATG	703
Qy	720	TCAGACGCAGGGCCACATCA	AACTGACCGACTTTTGA	CTCTGCAAGAGTCTATCCATG	779
Db	704	TTAATCATCAAGTCATGTGA	AACTAAACAGCTTTGGCTATG	CAAGAAATCTATTCATG	763
Qy	780	AGGGCGCGCTACTACAC	CTTCTGCGGACCATTTGATCATG	AGCCCTCAGATTCTG	839
Db	764	ATGGAACAGTACACACACAT	TTTGTGTGAACATAGATACATG	CCCCCTGAATCTTGA	823
Qy	840	TGCGCAGTGGCCACACAC	CGGCGCTGTGACTGTGAG	CGCTGGGGCCCTGATGTACACA	899
Db	824	TGAAGAGTGGCCACATCT	GTGCTGTGATTTGTGTGAAGTTTGG	AGCACTTAATGTATGACA	883
Qy	900	TGCTCATCTGATGTGCG	CGCGCTTTTACCGCAGAGAAC	CCGGAAGAAACCATGATTAATCA	959
Db	884	TGCTGACTGGAGCACCC	CAATTCACTGTGGAGAAATAGAA	AAACAATTAAGACAAATTC	943
Qy	960	TCAGGGGCAAGCTGAC	TAATGCCCCCTTACCTCAC	CCCGAGATGCCCCGGGACCTTGTCAAA	1019
Db	944	TCAAATGTAACTCAATTT	GTCTCTCCCTACCTCA	CTCAACAAAGACCAAGATCTGCTTAA	1003
Qy	1020	AGTTCTGAAACGGAATCC	ACAGCGGATTTGGGGTGGCC	CAAGGGAATGCTGTGAATG	1079
Db	1004	AGCTGCTGAATAAAGAAAT	GTGCTTCTGTGGAGCTG	CGTCTGGGAGCGCTGGAAG	1063
Qy	1080	TGCAAGACATCCCTTTT	CCGGAACATGAATTTGGGA	AGACCTCTTGGCGCTGGCGTGTG	1139
Db	1064	TTCAAGCTCATCTCAATCT	TTTAGACACATTAAC	TGGAAGAACTTCTGTGCTGAAAGGTG	1123
Qy	1140	ACCCCTCTTCAGGAC	CCCTGTCTGTGACATCA	AGAGACGTGAGCCAGTTGATACCCGCT	1199
Db	1124	AGCCCTCTTTAAAC	CTCTGTGTGCAATCTGA	AGAGAGTGAATGAAGTCACAGTTGATCTCAAGT	1183
Qy	1200	TCACACGGCAGAGCG	CGGTGGACAGTCTGTATGA	CAAGCCCTCAGGAGAGTSCAAC	1259
Db	1184	TTACACGTTCAGAC	ACTGTGCAGACGCC	CAAGTACCTAATCTTACGTGAAGATGCCAATC	1243
Qy	1260	AGGCTTCTGGGCTTCA	CATACGTGGCGCGCTGTGCT	CTGGAACGATCAAGAGGCGCT	1319
Db	1244	AGGCTTCTTGGGTTTAA	CAATGTGCTCCATCTGTAT	GTGAAGTGAAGTGAAGAAAGT	1303
Qy	1320	TCTCTCTTCAC	CCCCAAGTGGCTCAC	CCACAGGCGCTCAACAGTAAAGCCCGGCTCCCG	1379
Db	1304	TTTCTCTTTGAAC	CAAAATCGAATCA	CACTCGAAGATTTATTTGGAGCCCAAGAACACTG	1363
Qy	1380	TCAGCCCCCTCAAG	TTCTCCCTTTTGA	1407	
Db	1364	TCAGCCCAAGTCAATTTT	CTCTGGGGA	1391	

RESULT 13


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Db      632 GTGGAAGCTCTTACACAGATTGTTCTTAACAGAACCAATTCATTTGGGCTTTCTTC 691
Qy      629 -----TGTCTTACCTGGCTAGATCAAGCTGGGCTGGGCAATCTCCACAGG 681
Db      692 CTGGAATGCTTTTACTTGGGAGAAATCTCCATGCTTTGGGCAATTTACCAAAAGG 751
Qy      682 CATCATCTACCGGAGCTCAAGCCGAGAAATCATGCTCAGCAGCCAGGCAATCAA 741
Db      752 GATCATCTACAGAGACCTGAAGCCGAGAAATCATGCTTAAATCAACAGGCTCATGTGA 811
Qy      742 ACTGACCGACTTTGAGCTCTGCAAGAGCTTATCCATGAGGCGCGCTCATCAACCTT 801
Db      812 ACTAACAACCTTTGAGCTATGCAAGAAATTTATTCATGAGAACGTACACACACAT 871
Qy      802 CTGCGGACCATTTAGATACATGAGCCCTGAGATTCGTGCGCAGTGGCACAACCGAGG 861
Db      872 TTGTGGAACATGATATACATGAGCCCTGAAATCTTATGAGAAAGTGGCACAATGTGC 931
Qy      862 TGTGACCTGTGAGAGCTGGGCGCTCTGATGTAACGACATGCTCACTGATTCGCGCTT 921
Db      932 TGTGATGTTGTGAGTTTGGAGCATTAATGATGACATGCTGACCTGGAGCACCCCAT 991
Qy      922 TACCGACAGAAACCGAGAAACCAATGATTAATGATCATAGGCGCAGCTGCACTGCC 981
Db      992 CATGCGGAGAAATGAGAAAGAAACATTTGACAAATCTCTCAATGTAATCTCAATTTGCC 1051
Qy      982 CCGCTTACCTTACCCCATGATGCGCGGACCTTTGCAAAAGTTTCTGAAAACGAAATCCAG 1041
Db      1052 TCCTTACCTTACCAAGAAAGCCAGAGATCTGCTTAAAGCTGTGAAAAGAAAGTGGC 1111
Qy      1042 CCAGCGGATTTGGGCGTGGCCACAGGAGATCTGCTGATGTCAGAGACATCCCTTTTCCG 1101
Db      1112 TTCTCTCTGAGAGAGCTGTCTGAGGACGCTGAGAAAGTTCAAGCTCATTCATTTCTTAA 1171
Qy      1102 GCAATGATTTGGAGACACTTCTGAGCTGTGAGACCCCTTTTCAAGGCTGTCT 1161
Db      1172 ACACATTAATCTGGAGAAAGCTTCTGCTGAGAAAGTGGAGCCCTTTTAAACCTCTGT 1231
Qy      1162 GCGATCAGAGAGAGAGTGAAGCTGAGGATTTGATACCGCTTCAACGCGCAGACGCGGTGA 1221
Db      1232 GCATTTGAGAGAGATGTAAGTGAATTTGATTTCAAGTTTACAGCTCAGACACCTGTGA 1291
Qy      1222 CAGTCTGATGACACAGCCCTCAGCAGAGTGCACACAGGCTTCTGAGGCTTCAATA 1281
Db      1292 CAGCCCAAGATGACTCACTCTCAGTGAAGTGCACATCAGTCTTCTGAGGTTTAAATA 1351
Qy      1282 CGTGGGCGGCTGTCTCTGGAAGCAATCAAGAGGCGCTTCTCTTCCAGCCCAAGCTGG 1341
Db      1352 TGTGGCTCAGTCTGTCTTGAAGTGAAGTGAAGAAAGTTTCTTGAACCAAAATCCG 1411
Qy      1342 CTGACCCAGGCGCTCAACAGTAGCCCGCGGCTCCCGTCAAGCCCTCAAGTTCTCCG 1401
Db      1412 ATACCTCGAAGATTTATTGGCAGCCCAAGAACCTGTCAAGCCAGTCAAAATTTCTCC 1471
Qy      1402 TTTTGA 1407
Db      1472 TGGGGA 1477

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RESULT 15

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US-09-817-310-1
; Sequence 1, Application US/09817310
; Patent No. US20010042254A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Mary
; APPLICANT: Kozma, Sarah
; APPLICANT: Thomas, George
; TITLE OF INVENTION: Drosophila melanogaster P70 S6 Kinase
; FILE REFERENCE: 4-20971/A
; CURRENT APPLICATION NUMBER: US/09/817,310
; PRIOR APPLICATION NUMBER: 09/230,247
; PRIOR FILING DATE: 1999-04-16

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2556
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-817-310-1

Query Match      28.3%; Score 514; DB 9; Length 2556;
Best Local Similarity 67.9%; Pred. No. 3,8e-128;
Matches 718; Conservative 0; Mismatches 340; Indels 0; Gaps 0;

Qy      261 AGCTGACGAGACCAAGCTGAGACCTTGGCCCAAGAGCCGATGGGCGCCACTGCTTTAGC 320
Db      649 AGCTTGGAGAGAGATTTATCCAGGTAAATCAAGCTGAGACCCCAAGACCTTTAGC 708
Qy      321 TGTGCTGTGCTGTGGCAGAGGGGCTATGCAAGTGTTCAGGTGCGAAAGTGCAG 380
Db      709 TCAGAAAGTCTTTGGCAAGGCGGTATGCAAGTATTTCAAGTGGCAAGACCGCTG 768
Qy      381 GCACCAATTGGGCAAAATATATGCTCATGAAAGTCTTAAGAGGCCAAATTTGGCGCA 440
Db      769 GACGAGATGCTPAACAAATATTTTGCATGAAGTGTCTCAAAAGGCATTCATTTGACCA 828
Qy      441 ATGCCAAGACACAGACACACAGCGGCTGAGCGGAACTTCTAGTCACTGAAGCAC 500
Db      829 ATCAAAAGACACAGCGCACACCGCGCCGAGCCCAATATCTGAGGCAATGCAAGCATC 888
Qy      501 CTTTATTTGGAACTGGCTTATGCTTTCAGACTGTGTCGCAACTTACTTACTCTTCT 560
Db      889 CTTTATTTGGAGTGTGATTTATTTATGCTTTCAGACAGACGGAACCTATACCTTATCTG 948
Qy      561 AGTGCTGAGTGGGCGAGGCTTTCAGCATCTGAGCGAGGAGGCACTTCTTCTGAG 620
Db      949 AATATCTAGCGGTGAGAGAGCTTTCATGCAATTTGAGCGTGAAGGCACTTTTGAAG 1008
Qy      621 ATAGGCGCTTCTTACCTGCTGAGATACGCTGAGCCCTGAGCCATTTCACTCCAG 680
Db      1009 ATACCAACATCTTCTATATTAAGCAAAATCATTTTGGCTTGTGGCCATTTACCAAACTGG 1068
Qy      681 GCATCATTTACCGGAGCTCAAGCCCGAGAACATCATAGCTCAGACGCGAGGCGCATCA 740
Db      1069 GCATCATTTACCGGAGCTCAAGCCCGAGAACATCATAGCTCAGACGCGAGGCAATGGA 1128
Qy      741 AACTGACCGACTTTGAGCTTGAAGAGTGTATTCATGAGGCGCGCTCACTCACT 800
Db      1129 AGCTCAGGACTTTGAGCTTGAAGAGGACATTAAGAGGCTTATGTCAACCCACACT 1188
Qy      801 TGTGGGCAACATTTGAGTCAATGAGCCCTGAGATTTCTGTGCGCAGTGGCCACAACCGGG 860
Db      1189 TGTGGGCAACATTTGAGTCAATGAGCCTGAAATTTTGAACAGAGTGGCCATGAGCAAG 1248
Qy      861 CTGTGAGCTGTGAGCTGTGGGCGCTGATGTAAGCATGCTCACTGATTCGCGGCT 920
Db      1249 CAGTGAATGAGTGTGAGCTGTGGGCGCTCAGTGTGATGATGCTCAAGAGTCCACCT 1308
Qy      921 TTACCGCAGAGAACCGGAAGAAATCATGATTAATCATAGGCGGCAAGCTGGACATG 980
Db      1309 TCACCGCGAAGATTCGAAAGAACCATGAGACCATTTCTGAACCAAGCTCAATTTGC 1368
Qy      981 CCCCCTCACTCAACCCCAAGATCCCGGAGCTTGTCAAAAGTTTCTGAAACGGAATCCA 1040
Db      1369 CAGCTTACTCAACCCCAAGACCGAGGATCTGTGTCGTGCTGTGTAAGGCGGAGAAC 1428
Qy      1041 GCGACGCAATTTGGGAGTGGCCCAAGGAGATGCTGTGATGTCAGAGACATCCCTTTTCC 1100
Db      1429 CTGAGGCGCTTTGGACGCGGACCCAGAGATGGCGCGCTGTTCATAATACCACTTCTCA 1488
Qy      1101 GGCACATGAATTTGGACGACCTTCTGCGCTGCTGAGGACCCCTTTCAAGCCCTGTC 1160
Db      1489 AACAGCTGAATGAGGAGATGTGTGCAAGCGCTGAGACCGCTTATAAACCGGCTCT 1548
Qy      1161 TGCAGTCAAGAGAGAGCTGAGACCATTTGATACCCGCTTCAACAGGCAAGCGCGGTG 1220

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Db 1549 TGAGAGGAGGATGATGTCTCACAGTTGATACAGATTTCACAGACAAATTCCAGTGG 1608
QY 1221 ACAATCCTGATGAGACAGAGCCCTCAGAGAGATGSCCAACAGGCCCTTCTGGGCTTGACAT 1280
Db 1609 ATTCCCTGATGATACAGCTTAAGCGAAGTGCCTTAATTTCOAAGTTTCACCT 1668
QY 1281 ACCTGGGCGCCGCTCTGCTCGAGACAGCATCAAGAGAGGC 1318
Db 1669 ACCTTGACACCTCGATACCTGAGAGATATGATCGGGCC 1706

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